

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Abrams, Mark A.
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Caparon, Maire H.
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Klein, Barbara K.
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Olins, Peter O.
Paik, Kumman
Thomas, John W.

(ii) TITLE OF INVENTION: Methods Of Ex-Vivo Expansion Of Hematopoietic Cells Using Multivariant (IL-3) Hematopoiesis Chimera Proteins

(iii) NUMBER OF SEQUENCES: 197

(iv) CORRESPONDENCE ADDRESS:

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(C) CITY: St. Louis
(D) STATE: Missouri
(E) COUNTRY: USA
(F) ZIP: 63167

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: not assigned
(B) FILING DATE: 22-FEB-2002
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 08/762,227
(B) FILING DATE: 09-DEC-1996

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/192,325
(B) FILING DATE: 14-FEB-1994

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/446,872
(B) FILING DATE: 06-JUN-1995

(viii) ATTORNEY/AGENT INFORMATION:

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(C) REFERENCE/DOCKET NUMBER: C-2790/6

(ix) TELECOMMUNICATION INFORMATION:

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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 133 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1
- (D) OTHER INFORMATION: /note= "Met- may or may not precede the amino acid in position 1"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 17
- (D) OTHER INFORMATION: /note= "Xaa at position 17 is Ser, Lys, Gly, Asp, Met, Gln, or Arg"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 18
- (D) OTHER INFORMATION: /note= "Xaa at position 18 is Asn, His, Leu, Ile, Phe, Arg, or Gln"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 19
- (D) OTHER INFORMATION: /note= "Xaa at position 19 is Met, Phe, Ile, Arg, Gly, Ala, or Cys"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 20
- (D) OTHER INFORMATION: /note= "Xaa at position 20 is Ile, Cys, Gln, Glu, Arg, Pro, or Ala"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 21
- (D) OTHER INFORMATION: /note= "Xaa at position 21 is Asp, Phe, Lys, Arg, Ala, Gly, Glu, Gln, Asn, Thr, Ser, or Val"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 22
- (D) OTHER INFORMATION: /note= "Xaa at position 22 is Glu, Trp, Pro, Ser, Ala, His, Asp, Asn, Gln, Leu, Val, or Gly"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 23
- (D) OTHER INFORMATION: /note= "Xaa at position 23 is Ile,"

Val, Ala, Leu, Gly, Trp, Lys, Phe, Ser, or Arg"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 24
- (D) OTHER INFORMATION: /note= "Xaa at position 24 is Ile, Gly, Val, Arg, Ser, Phe, or Leu"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 25
- (D) OTHER INFORMATION: /note= "Xaa at position 25 is Thr, His, Gly, Gln, Arg, Pro, or Ala"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 26
- (D) OTHER INFORMATION: /note= "Xaa at position 26 is His, Thr, Phe, Gly, Arg, Ala, or Trp"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 27
- (D) OTHER INFORMATION: /note= "Xaa at position 27 is Leu, Gly, Arg, Thr, Ser, or Ala"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 28
- (D) OTHER INFORMATION: /note= "Xaa at position 28 is Lys, Arg, Leu, Gln, Gly, Pro, Val, or Trp"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 29
- (D) OTHER INFORMATION: /note= "Xaa at position 29 is Gln, Asn, Leu, Pro, Arg, or Val"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 30
- (D) OTHER INFORMATION: /note= "Xaa at position 30 is Pro, His, Thr, Gly, Asp, Gln, Ser, Leu, or Lys"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 31
- (D) OTHER INFORMATION: /note= "Xaa at position 31 is Pro, Asp, Gly, Ala, Arg, Leu, or Gln"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 32
- (D) OTHER INFORMATION: /note= "Xaa at position 32 is Leu, Val, Arg, Gln, Asn, Gly, Ala, or Glu"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 33
- (D) OTHER INFORMATION: /note= "Xaa at position 33 is Pro,"

Leu, Gln, Ala, Thr, or Glu"

- (ix) FEATURE:
 - (A) NAME/KEY: Modified-site
 - (B) LOCATION: 34
 - (D) OTHER INFORMATION: /note= "Xaa at position 34 is Leu, Val, Gly, Ser, Lys, Glu, Gln, Thr, Arg, Ala, Phe, Ile, or Met"
- (ix) FEATURE:
 - (A) NAME/KEY: Modified-site
 - (B) LOCATION: 35
 - (D) OTHER INFORMATION: /note= "Xaa at position 35 is Leu, Ala, Gly, Asn, Pro, Gln, or Val"
- (ix) FEATURE:
 - (A) NAME/KEY: Modified-site
 - (B) LOCATION: 36
 - (D) OTHER INFORMATION: /note= "Xaa at position 36 is Asp, Leu, or Val"
- (ix) FEATURE:
 - (A) NAME/KEY: Modified-site
 - (B) LOCATION: 37
 - (D) OTHER INFORMATION: /note= "Xaa at position 37 is Phe, Ser, Pro, Trp, or Ile"
- (ix) FEATURE:
 - (A) NAME/KEY: Modified-site
 - (B) LOCATION: 38
 - (D) OTHER INFORMATION: /note= "Xaa at position 38 is Asn, or Ala"
- (ix) FEATURE:
 - (A) NAME/KEY: Modified-site
 - (B) LOCATION: 40
 - (D) OTHER INFORMATION: /note= "Xaa at position 40 is Leu, Trp, or Arg"
- (ix) FEATURE:
 - (A) NAME/KEY: Modified-site
 - (B) LOCATION: 41
 - (D) OTHER INFORMATION: /note= "Xaa at position 41 is Asn, Cys, Arg, Leu, His, Met, or Pro"
- (ix) FEATURE:
 - (A) NAME/KEY: Modified-site
 - (B) LOCATION: 42
 - (D) OTHER INFORMATION: /note= "Xaa at position 42 is Gly, Asp, Ser, Cys, Asn, Lys, Thr, Leu, Val, Glu, Phe, Tyr, Ile, Met, or Ala"
- (ix) FEATURE:
 - (A) NAME/KEY: Modified-site
 - (B) LOCATION: 43
 - (D) OTHER INFORMATION: /note= "Xaa at position 43 is Glu, Asn, Tyr, Leu, Phe, Asp, Ala, Cys, Gln, Arg, Thr, Gly, or Ser"
- (ix) FEATURE:
 - (A) NAME/KEY: Modified-site

(B) LOCATION: 44
(D) OTHER INFORMATION: /note= "Xaa at position 44 is Asp, Ser, Leu, Arg, Lys, Thr, Met, Trp, Glu, Asn, Gln, Ala, or Pro"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 45
(D) OTHER INFORMATION: /note= "Xaa at position 45 is Gln, Pro, Phe, Val, Met, Leu, Thr, Lys, Trp, Asp, Asn, Arg, Ser, Ala, Ile, Glu, or His"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 46
(D) OTHER INFORMATION: /note= "Xaa at position 46 is Asp, Phe, Ser, Thr, Cys, Glu, Asn, Gln, Lys, His, Ala, Tyr, Ile, Val, or Gly"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 47
(D) OTHER INFORMATION: /note= "Xaa at position 47 is Ile, Gly, Val, Ser, Arg, Pro, or His"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 48
(D) OTHER INFORMATION: /note= "Xaa at position 48 is Leu, Ser, Cys, Arg, Ile, His, Phe, Glu, Lys, Thr, Ala, Met, Val, or Asn"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 49
(D) OTHER INFORMATION: /note= "Xaa at position 49 is Met, Arg, Ala, Gly, Pro, Asn, His, or Asp"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 50
(D) OTHER INFORMATION: /note= "Xaa at position 50 is Glu, Leu, Thr, Asp, Tyr, Lys, Asn, Ser, Ala, Ile, Val, His, Phe, Met, or Gln"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 51
(D) OTHER INFORMATION: /note= "Xaa at position 51 is Asn, Arg, Met, Pro, Ser, Thr, or His"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 52
(D) OTHER INFORMATION: /note= "Xaa at position 52 is Asn, His, Arg, Leu, Gly, Ser, or Thr"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 53
(D) OTHER INFORMATION: /note= "Xaa at position 53 is

Leu, Thr, Ala, Gly, Glu, Pro, Lys, Ser, or Met"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 54
- (D) OTHER INFORMATION: /note= "Xaa at position 54 is Arg, Asp, Ile, Ser, Val, Thr, Gln, Asn, Lys, His, Ala, or Leu"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 55
- (D) OTHER INFORMATION: /note= "Xaa at position 55 is Arg, Thr, Val, Ser, Leu, or Gly"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 56
- (D) OTHER INFORMATION: /note= "Xaa at position 56 is Pro, Gly, Cys, Ser, Gln, Glu, Arg, His, Thr, Ala, Tyr, Phe, Leu, Val, or Lys"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 57
- (D) OTHER INFORMATION: /note= "Xaa at position 57 is Asn or Gly"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 58
- (D) OTHER INFORMATION: /note= "Xaa at position 58 is Leu, Ser, Asp, Arg, Gln, Val, or Cys"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 59
- (D) OTHER INFORMATION: /note= "Xaa at position 59 is Glu, Tyr, His, Leu, Pro, or Arg"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 60
- (D) OTHER INFORMATION: /note= "Xaa at position 60 is Ala, Ser, Pro, Tyr, Asn, or Thr"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 61
- (D) OTHER INFORMATION: /note= "Xaa at position 61 is Phe, Asn, Glu, Pro, Lys, Arg, or Ser"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 62
- (D) OTHER INFORMATION: /note= "Xaa at position 62 is Asn, His, Val, Arg, Pro, Thr, Asp, or Ile"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 63

(D) OTHER INFORMATION: /note= "Xaa at position 63 is Arg, Tyr, Trp, Lys, Ser, His, Pro, or Val"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 64
(D) OTHER INFORMATION: /note= "Xaa at position 64 is Ala, Asn, Pro, Ser, or Lys"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 65
(D) OTHER INFORMATION: /note= "Xaa at position 65 is Val, Thr, Pro, His, Leu, Phe, or Ser"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 66
(D) OTHER INFORMATION: /note= "Xaa at position 66 is Lys, Ile, Arg, Val, Asn, Glu, or Ser"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 67
(D) OTHER INFORMATION: /note= "Xaa at position 67 is Ser, Ala, Phe, Val, Gly, Asn, Ile, Pro, or His"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 68
(D) OTHER INFORMATION: /note= "Xaa at position 68 is Leu, Val, Trp, Ser, Ile, Phe, Thr, or His"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 69
(D) OTHER INFORMATION: /note= "Xaa at position 69 is Gln, Ala, Pro, Thr, Glu, Arg, Trp, Gly, or Leu"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 70
(D) OTHER INFORMATION: /note= "Xaa at position 70 is Asn, Leu, Val, Trp, Pro, or Ala"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 71
(D) OTHER INFORMATION: /note= "Xaa at position 71 is Ala, Met, Leu, Pro, Arg, Glu, Thr, Gln, Trp, or Asn"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 72
(D) OTHER INFORMATION: /note= "Xaa at position 72 is Ser, Glu, Met, Ala, His, Asn, Arg, or Asp"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 73

(D) OTHER INFORMATION: /note= "Xaa at position 73 is Ala, Glu, Asp, Leu, Ser, Gly, Thr, or Arg"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 74

(D) OTHER INFORMATION: /note= "Xaa at position 74 is Ile, Met, Thr, Pro, Arg, Gly, or Ala"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 75

(D) OTHER INFORMATION: /note= "Xaa at position 75 is Glu, Lys, Gly, Asp, Pro, Trp, Arg, Ser, Gln, or Leu"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 76

(D) OTHER INFORMATION: /note= "Xaa at position 76 is Ser, Val, Ala, Asn, Trp, Glu, Pro, Gly, or Asp"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 77

(D) OTHER INFORMATION: /note= "Xaa at position 77 is Ile, Ser, Arg, Thr, or Leu"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 78

(D) OTHER INFORMATION: /note= "Xaa at position 78 is Leu, Ala, Ser, Glu, Phe, Gly, or Arg"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 79

(D) OTHER INFORMATION: /note= "Xaa at position 79 is Lys, Thr, Asn, Met, Arg, Ile, Gly, or Asp"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 80

(D) OTHER INFORMATION: /note= "Xaa at position 80 is Asn, Trp, Val, Gly, Thr, Leu, Glu, or Arg"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 81

(D) OTHER INFORMATION: /note= "Xaa at position 81 is Leu, Gln, Gly, Ala, Trp, Arg, Val, or Lys"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 82

(D) OTHER INFORMATION: /note= "Xaa at position 82 is Leu, Gln, Lys, Trp, Arg, Asp, Glu, Asn, His, Thr, Ser, Ala, Tyr, Phe, Ile, Met, or Val"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 83
(D) OTHER INFORMATION: /note= "Xaa at position 83 is Pro, Ala, Thr, Trp, Arg, or Met"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 84
(D) OTHER INFORMATION: /note= "Xaa at position 84 is Cys, Glu, Gly, Arg, Met, or Val"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 85
(D) OTHER INFORMATION: /note= "Xaa at position 85 is Leu, Asn, Val, or Gln"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 86
(D) OTHER INFORMATION: /note= "Xaa at position 86 is Pro, Cys, Arg, Ala, or Lys"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 87
(D) OTHER INFORMATION: /note= "Xaa at position 87 is Leu, Ser, Trp, or Gly"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 88
(D) OTHER INFORMATION: /note= "Xaa at position 88 is Ala, Lys, Arg, Val, or Trp"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 89
(D) OTHER INFORMATION: /note= "Xaa at position 89 is Thr, Asp, Cys, Leu, Val, Glu, His, Asn, or Ser"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 90
(D) OTHER INFORMATION: /note= "Xaa at position 90 is Ala, Pro, Ser, Thr, Gly, Asp, Ile, or Met"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 91
(D) OTHER INFORMATION: /note= "Xaa at position 91 is Ala, Pro, Ser, Thr, Phe, Leu, Asp, or His"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 92
(D) OTHER INFORMATION: /note= "Xaa at position 92 is Pro, Phe, Arg, Ser, Lys, His, Ala, Gly, Ile, or Leu"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 93

(D) OTHER INFORMATION: /note= "Xaa at position 93 is Thr, Asp, Ser, Asn, Pro, Ala, Leu, or Arg"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 94

(D) OTHER INFORMATION: /note= "Xaa at position 94 is Arg, Ile, Ser, Glu, Leu, Val, Gln, Lys, His, Ala, or Pro"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 95

(D) OTHER INFORMATION: /note= "Xaa at position 95 is His, Gln, Pro, Arg, Val, Leu, Gly, Thr, Asn, Lys, Ser, Ala, Trp, Phe, Ile, or Tyr"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 96

(D) OTHER INFORMATION: /note= "Xaa at position 96 is Pro, Lys, Tyr, Gly, Ile, or Thr"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 97

(D) OTHER INFORMATION: /note= "Xaa at position 97 is Ile, Val, Lys, Ala, or Asn"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 98

(D) OTHER INFORMATION: /note= "Xaa at position 98 is His, Ile, Asn, Leu, Asp, Ala, Thr, Glu, Gln, Ser, Phe, Met, Val, Lys, Arg, Tyr, or Pro"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 99

(D) OTHER INFORMATION: /note= "Xaa at position 99 is Ile, Leu, Arg, Asp, Val, Pro, Gln, Gly, Ser, Phe, or His"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 100

(D) OTHER INFORMATION: /note= "Xaa at position 100 is Lys, Tyr, Leu, His, Arg, Ile, Ser, Gln, or Pro"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 101

(D) OTHER INFORMATION: /note= "Xaa at position 101 is Asp, Pro, Met, Lys, His, Thr, Val, Tyr, Glu, Asn, Ser, Ala, Gly, Ile, Leu, or Gln"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 102

(D) OTHER INFORMATION: /note= "Xaa at position 102 is Gly, Leu, Glu, Lys, Ser, Tyr, or Pro"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 103
(D) OTHER INFORMATION: /note= "Xaa at position 103 is Asp, or Ser"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 104
(D) OTHER INFORMATION: /note= "Xaa at position 104 is Trp, Val, Cys, Tyr, Thr, Met, Pro, Leu, Gln, Lys, Ala, Phe, or Gly"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 105
(D) OTHER INFORMATION: /note= "Xaa at position 105 is Asn, Pro, Ala, Phe, Ser, Trp, Gln, Tyr, Leu, Lys, Ile, Asp, or His"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 106
(D) OTHER INFORMATION: /note= "Xaa at position 106 is Glu, Ser, Ala, Lys, Thr, Ile, Gly, or Pro"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 108
(D) OTHER INFORMATION: /note= "Xaa at position 108 is Arg, Lys, Asp, Leu, Thr, Ile, Gln, His, Ser, Ala, or Pro"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 109
(D) OTHER INFORMATION: /note= "Xaa at position 109 is Arg, Thr, Pro, Glu, Tyr, Leu, Ser, or Gly"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 110
(D) OTHER INFORMATION: /note= "Xaa at position 110 is Lys, Ala, Asn, Thr, Leu, Arg, Gln, His, Glu, Ser, or Trp"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 111
(D) OTHER INFORMATION: /note= "Xaa at position 111 is Leu, Ile, Arg, Asp, or Met"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 112
(D) OTHER INFORMATION: /note= "Xaa at position 112 is Thr, Val, Gln, Tyr, Glu, His, Ser, or Phe"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 113
(D) OTHER INFORMATION: /note= "Xaa at position 113 is Phe, Ser, Cys, His, Gly, Trp, Tyr, Asp, Lys, Leu, Ile, Val,

or Asn"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 114
- (D) OTHER INFORMATION: /note= "Xaa at position 114 is Tyr, Cys, His, Ser, Trp, Arg, or Leu"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 115
- (D) OTHER INFORMATION: /note= "Xaa at position 115 is Leu, Asn, Val, Pro, Arg, Ala, His, Thr, Trp, or Met"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 116
- (D) OTHER INFORMATION: /note= "Xaa at position 116 is Lys, Leu, Pro, Thr, Met, Asp, Val, Glu, Arg, Trp, Ser, Asn, His, Ala, Tyr, Phe, Gln, or Ile"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 117
- (D) OTHER INFORMATION: /note= "Xaa at position 117 is Thr, Ser, Asn, Ile, Trp, Lys, or Pro"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 118
- (D) OTHER INFORMATION: /note= "Xaa at position 118 is Leu, Ser, Pro, Ala, Glu, Cys, Asp, or Tyr"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 119
- (D) OTHER INFORMATION: /note= "Xaa at position 119 is Glu, Ser, Lys, Pro, Leu, Thr, Tyr, or Arg"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 120
- (D) OTHER INFORMATION: /note= "Xaa at position 120 is Asn, Ala, Pro, Leu, His, Val, or Gln"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 121
- (D) OTHER INFORMATION: /note= "Xaa at position 121 is Ala, Ser, Ile, Asn, Pro, Lys, Asp, or Gly"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 122
- (D) OTHER INFORMATION: /note= "Xaa at position 122 is Gln, Ser, Met, Trp, Arg, Phe, Pro, His, Ile, Tyr, or Cys"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site

(B) LOCATION: 123

(D) OTHER INFORMATION: /note= "Xaa at position 123 is Ala,
Met, Glu, His, Ser, Pro, Tyr, or Leu"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Ala	Pro	Met	Thr	Gln	Thr	Thr	Ser	Leu	Lys	Thr	Ser	Trp	Val	Asn	Cys
1				5				10					15		
Xaa															
								25					30		
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Asn	Xaa								
						35		40					45		
Xaa															
						50		55					60		
Xaa															
						65		70					75		80
Xaa															
						85		90					95		
Xaa	Phe	Xaa	Xaa	Xaa	Xaa										
						100		105					110		
Xaa	Gln	Gln	Thr	Thr	Leu										
						115		120					125		
Ser	Leu	Ala	Ile	Phe											
				130											

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 133 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1
- (D) OTHER INFORMATION: /note= "Met- may or may not precede the amino acid in position 1"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 17
- (D) OTHER INFORMATION: /note= "Xaa at position 17 is Ser, Gly, Asp, Met, or Gln"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 18
- (D) OTHER INFORMATION: /note= "Xaa at position 18 is Asn, His, or Ile"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 19
(D) OTHER INFORMATION: /note= "Xaa at position 19 is Met or Ile"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 21
(D) OTHER INFORMATION: /note="Xaa at position 21 is Asp or Glu"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 23
(D) OTHER INFORMATION: /note= "Xaa at position 23 is Ile, Ala, Leu, or Gly"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 24
(D) OTHER INFORMATION: /note= "Xaa at position 24 is Ile, Val, or Leu"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 25
(D) OTHER INFORMATION: /note= "Xaa at position 25 is Thr, His, Gln, or Ala"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 26
(D) OTHER INFORMATION: /note= "Xaa at position 26 is His or Ala"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 29
(D) OTHER INFORMATION: /note= "Xaa at position 29 is Gln, Asn, or Val"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 30
(D) OTHER INFORMATION: /note= "Xaa at position 30 is Pro, Gly, or Gln"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 31
(D) OTHER INFORMATION: /note= "Xaa at position 31 is Pro, Asp, Gly, or Gln"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 32
(D) OTHER INFORMATION: /note= "Xaa at position 32 is Leu, Arg, Gln, Asn, Gly, Ala, or Glu"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 33
(D) OTHER INFORMATION: /note= "Xaa at position 33 is Pro or Glu"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 34
(D) OTHER INFORMATION: /note= "Xaa at position 34 is Leu, Val, Gly, Ser, Lys, Ala, Arg, Gln, Glu, Ile, Phe, Thr, or Met"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 35
(D) OTHER INFORMATION: /note= "Xaa at position 35 is Leu, Ala, Asn, Pro, Gln, or Val"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 37
(D) OTHER INFORMATION: /note= "Xaa at position 37 is Phe, Ser, Pro, or Trp"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 38
(D) OTHER INFORMATION: /note= "Xaa at position 38 is Asn or Ala"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 42
(D) OTHER INFORMATION: /note= "Xaa at position 42 is Gly, Asp, Ser, Cys, Ala, Asn, Ile, Leu, Met, Tyr, or Arg"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 44
(D) OTHER INFORMATION: /note= "Xaa at position 44 is Asp or Glu"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 45
(D) OTHER INFORMATION: /note= "Xaa at position 45 is Gln, Val, Met, Leu, Thr, Ala, Asn, Glu, Ser, or Lys"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 46
(D) OTHER INFORMATION: /note= "Xaa at position 46 is Asp, Phe, Ser, Thr, Ala, Asn, Gln, Glu, His, Ile, Lys, Tyr, Val, or Cys"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 50
(D) OTHER INFORMATION: /note= "Xaa at position 50 is Glu, Ala, Asn, Ser, or Asp"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 51
(D) OTHER INFORMATION: /note= "Xaa at position 51 is Asn, Arg, Met, Pro, Ser, Thr, or His"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 54
(D) OTHER INFORMATION: /note="Xaa at position 54 is Arg or Ala"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 55
(D) OTHER INFORMATION: /note= "Xaa at position 55 is Arg, Thr, Val, Leu, or Gly"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 56
(D) OTHER INFORMATION: /note= "Xaa at position 56 is Pro, Gly, Ser, Gln, Ala, Arg, Asn, Glu, Leu, Thr, Val, or Lys"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 60
(D) OTHER INFORMATION: /note= "Xaa at position 60 is Ala or Ser"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 62
(D) OTHER INFORMATION: /note= "Xaa at position 62 is Asn, Pro, Thr, or Ile"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 63
(D) OTHER INFORMATION: /note= "Xaa at position 63 is Arg or Lys"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 64
(D) OTHER INFORMATION: /note= "Xaa at position 64 is Ala or Asn"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 65
(D) OTHER INFORMATION: /note= "Xaa at position 65 is Val or Thr"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 66
(D) OTHER INFORMATION: /note= "Xaa at position 66 is Lys or Arg"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 67
(D) OTHER INFORMATION: /note= "Xaa at position 67 is Ser
Phe or His"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 68
(D) OTHER INFORMATION: /note= "Xaa at position 68 is Leu,
Ile, Phe, or His"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 69
(D) OTHER INFORMATION: /note= "Xaa at position 69 is Gln,
Ala, Pro, Thr, Glu, Arg, or Gly"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 71
(D) OTHER INFORMATION: /note= "Xaa at position 71 is Ala,
Pro, or Arg"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 72
(D) OTHER INFORMATION: /note= "Xaa at position 72 is Ser,
Glu, Arg, or Asp"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 73
(D) OTHER INFORMATION: /note= "Xaa at position 73 is Ala
or Leu"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 76
(D) OTHER INFORMATION: /note= "Xaa at position 76 is Ser,
Val, Ala, Asn, Glu, Pro, or Gly"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 77
(D) OTHER INFORMATION: /note= "Xaa at position 77 is Ile
or Leu"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 79
(D) OTHER INFORMATION: /note= "Xaa at position 79 is
Lys, Thr, Gly, Asn, Met, Arg, Ile, or Asp"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 80
(D) OTHER INFORMATION: /note= "Xaa at position 80 is Asn,
Gly, Glu, or Arg"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 82
(D) OTHER INFORMATION: /note= "Xaa at position 82 is Leu,
Gln, Trp, Arg, Asp, Ala, Asn, Glu, His, Ile,
Met, Phe, Ser, Thr, Tyr, or Val"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 83
(D) OTHER INFORMATION: /note= "Xaa at position 83 is Pro
or Thr"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 85
(D) OTHER INFORMATION: /note= "Xaa at position 85 is Leu
or Val"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 87
(D) OTHER INFORMATION: /note= "Xaa at position 87 is Leu
or Ser"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 88
(D) OTHER INFORMATION: /note= "Xaa at position 88 is Ala
or Trp"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 91
(D) OTHER INFORMATION: /note= "Xaa at position 91 is Ala
or Pro"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 93
(D) OTHER INFORMATION: /note= "Xaa at position 93 is Thr,
Asp, Ser, Pro, Ala, Leu, or Arg"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 95
(D) OTHER INFORMATION: /note= "Xaa at position 95 is His,
Pro, Arg, Val, Leu, Gly, Asn, Phe, Ser, or Thr"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 96
(D) OTHER INFORMATION: /note= "Xaa at position 96 is Pro
or Tyr"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 97
(D) OTHER INFORMATION: /note= "Xaa at position 97 is Ile
or Val"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 98
(D) OTHER INFORMATION: /note= "Xaa at position 98 is His,
Ile, Asn, Leu, Ala, Thr, Arg, Gln, Lys,
Met, Ser, Tyr, Val, or Pro"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 99
(D) OTHER INFORMATION: /note= "Xaa at position 99 is Ile,
Leu, or Val"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 100
(D) OTHER INFORMATION: /note= "Xaa at position 100 is Lys,
Arg, Ile, Gln, Pro, or Ser"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 101
(D) OTHER INFORMATION: /note= "Xaa at position 101 is Asp,
Pro, Met, Lys, Thr, His, Asn, Ile, Leu, or Tyr"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 104
(D) OTHER INFORMATION: /note= "Xaa at position 104 is Trp
or Leu"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 105
(D) OTHER INFORMATION: /note= "Xaa at position 105 is
Asn, Pro, Ala, Ser, Trp, Gln, Tyr, Leu, Lys, Ile,
Asp, or His"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 106
(D) OTHER INFORMATION: /note= "Xaa at position 106 is Glu
or Gly"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 108
(D) OTHER INFORMATION: /note="Xaa at position 108 is Arg,
Ala, or Ser"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 109
(D) OTHER INFORMATION: /note= "Xaa at position 109 is Arg,
Thr, Glu, Leu, or Ser"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 112
(D) OTHER INFORMATION: /note= "Xaa at position 112 is Thr,
Val, or Gln"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 114
(D) OTHER INFORMATION: /note= "Xaa at position 114 is Tyr or Trp"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 115
(D) OTHER INFORMATION: /note= "Xaa at position 115 is Leu or Ala"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 116
(D) OTHER INFORMATION: /note= "Xaa at position 116 is Lys, Thr, Val, Trp, Ser, Ala, His, Met, Phe, Tyr, or Ile"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 117
(D) OTHER INFORMATION: /note= "Xaa at position 117 is Thr or Ser"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 120
(D) OTHER INFORMATION: /note= "Xaa at position 120 is Asn, Pro, Leu, His, Val, or Gln"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 121
(D) OTHER INFORMATION: /note= "Xaa at position 121 is Ala, Ser, Ile, Asn, Pro, Asp, or Gly"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 122
(D) OTHER INFORMATION: /note= "Xaa at position 122 is Gln, Ser, Met, Trp, Arg, Phe, Pro, His, Ile, Tyr, or Cys"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 123
(D) OTHER INFORMATION: /note= "Xaa at position 123 is Ala, Met, Glu, His, Ser, Pro, Tyr, or Leu"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Ala Pro Met Thr Gln Thr Thr Ser Leu Lys Thr Ser Trp Val Asn Cys
1 5 10 15

Xaa Xaa Xaa Ile Xaa Glu Xaa Xaa Xaa Xaa Leu Lys Xaa Xaa Xaa Xaa
20 25 30

Xaa Xaa Xaa Asp Xaa Xaa Asn Leu Asn Xaa Glu Xaa Xaa Xaa Ile Leu
35 40 45

Met Xaa Xaa Asn Leu Xaa Xaa Xaa Asn Leu Glu Xaa Phe Xaa Xaa Xaa
50 55 60

Xaa Xaa Xaa Xaa Xaa Asn Xaa Xaa Xaa Ile Glu Xaa Xaa Leu Xaa Xaa
65 70 75 80

Leu Xaa Xaa Cys Xaa Pro Xaa Xaa Thr Ala Xaa Pro Xaa Arg Xaa Xaa
85 90 95

Xaa Xaa Xaa Xaa Xaa Gly Asp Xaa Xaa Xaa Phe Xaa Xaa Lys Leu Xaa
100 105 110

Phe Xaa Xaa Xaa Xaa Leu Glu Xaa Xaa Xaa Gln Gln Thr Thr Leu
115 120 125

Ser Leu Ala Ile Phe
130

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 133 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1
- (D) OTHER INFORMATION: /note= "Met- may or may not precede the amino acid in position 1"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 17
- (D) OTHER INFORMATION: /note= "Xaa at position 17 is Ser, Gly, Asp, or Gln"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 18
- (D) OTHER INFORMATION: /note= "Xaa at position 18 is Asn, His, or Ile"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 23
- (D) OTHER INFORMATION: /note= "Xaa at position 23 is Ile, Ala, Leu, or Gly"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 25
- (D) OTHER INFORMATION: /note= "Xaa at position 25 is Thr, His, or Gln"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 26
- (D) OTHER INFORMATION: /note= "Xaa at position 26 is His or Ala"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 29
- (D) OTHER INFORMATION: /note="Xaa at position 29 is Gln or Asn"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 30
- (D) OTHER INFORMATION: /note= "Xaa at position 30 is Pro or Gly"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 32
- (D) OTHER INFORMATION: /note= "Xaa at position 32 is Leu, Arg, Asn, or Ala"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 34
- (D) OTHER INFORMATION: /note= "Xaa at position 34 is Leu, Val, Ser, Ala, Arg, Gln, Glu, Ile, Phe, Thr, or Met"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 35
- (D) OTHER INFORMATION: /note= "Xaa at position 35 is Leu, Ala, Asn, or Pro"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 38
- (D) OTHER INFORMATION: /note= "Xaa at position 38 is Asn or Ala"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 42
- (D) OTHER INFORMATION: /note= "Xaa at position 42 is Gly, Asp, Ser, Ala, Asn, Ile, Leu, Met, Tyr, or Arg"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 45
- (D) OTHER INFORMATION: /note= "Xaa at position 45 is Gln, Val, Met, Leu, Ala, Asn, Glu, or Lys"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 46
- (D) OTHER INFORMATION: /note= "Xaa at position 46 is Asp, Phe, Ser, Gln, Glu, His, Val, or Thr"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site

(B) LOCATION: 50
(D) OTHER INFORMATION: /note= "Xaa at position 50 is Glu, Asn, Ser, or Asp"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 51
(D) OTHER INFORMATION: /note= "Xaa at position 51 is Asn, Arg, Pro, Thr, or His"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 55
(D) OTHER INFORMATION: /note= "Xaa at position 55 is Arg, Leu, or Gly"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 56
(D) OTHER INFORMATION: /note= "Xaa at position 56 is Pro, Gly, Ser, Ala, Asn, Val, Leu, or Gln"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 62
(D) OTHER INFORMATION: /note= "Xaa at position 62 is Asn, Pro, or Thr"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 64
(D) OTHER INFORMATION: /note= "Xaa at position 64 is Ala or Asn"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 65
(D) OTHER INFORMATION: /note= "Xaa at position 65 is Val or Thr"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 67
(D) OTHER INFORMATION: /note= "Xaa at position 67 is Ser or Phe"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 68
(D) OTHER INFORMATION: /note= "Xaa at position 68 is Leu or Phe"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 69
(D) OTHER INFORMATION: /note= "Xaa at position 69 is Gln, Ala, Glu, or Arg"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 76

(D) OTHER INFORMATION: /note= "Xaa at position 76 is Ser, Val, Asn, Pro, or Gly"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 77
(D) OTHER INFORMATION: /note= "Xaa at position 77 is Ile or Leu"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 79
(D) OTHER INFORMATION: /note= "Xaa at position 79 is Lys, Asn, Met, Arg, Ile, or Gly"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 80
(D) OTHER INFORMATION: /note= "Xaa at position 80 is Asn, Gly, Glu, or Arg"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 82
(D) OTHER INFORMATION: /note= "Xaa at position 82 is Leu, Gln, Trp, Arg, Asp, Asn, Glu, His, Met, Phe, Ser, Thr, Tyr, or Val"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 87
(D) OTHER INFORMATION: /note= "Xaa at position 87 is Leu or Ser"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 88
(D) OTHER INFORMATION: /note= "Xaa at position 88 is Ala or Trp"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 91
(D) OTHER INFORMATION: /note= "Xaa at position 91 is Ala or Pro"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 93
(D) OTHER INFORMATION: /note= "Xaa at position 93 is Thr, Asp, or Ala"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 95
(D) OTHER INFORMATION: /note= "Xaa at position 95 is His, Pro, Arg, Val, Gly, Asn, Ser, or Thr"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 98

(D) OTHER INFORMATION: /note= "Xaa at position 98 is His, Ile, Asn, Ala, Thr, Gln, Glu, Lys, Met, Ser, Tyr, Val, or Leu"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 99
(D) OTHER INFORMATION: /note= "Xaa at position 99 is Ile or Leu"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 100
(D) OTHER INFORMATION: /note= "Xaa at position 100 is Lys or Arg"

(ix) FEATURE;
(A) NAME/KEY: Modified-site
(B) LOCATION: 101
(D) OTHER INFORMATION: /note= "Xaa at position 101 is Asp, Pro, Met, Lys, Thr, His, Asn, Ile, Leu, or Tyr"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 105
(D) OTHER INFORMATION: /note= "Xaa at position 105 is Asn, Pro, Ser, Ile, or Asp"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 108
(D) OTHER INFORMATION: /note= "Xaa at position 108 is Arg, Ala, or Ser"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 109
(D) OTHER INFORMATION: /note= "Xaa at position 109 is Arg, Thr, Glu, Leu, or Ser"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 112
(D) OTHER INFORMATION: /note= "Xaa at position 112 is Thr or Gln"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 116
(D) OTHER INFORMATION: /note= "Xaa at position 116 is Lys, Val, Trp, Ala, His, Phe, Tyr, or Ile"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 117
(D) OTHER INFORMATION: /note= "Xaa at position 117 is Thr or Ser"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 120
(D) OTHER INFORMATION: /note= "Xaa at position 120 is Asn,

Pro, Leu, His, Val, or Gln"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 121
- (D) OTHER INFORMATION: /note= "Xaa at position 121 is Ala, Ser, Ile, Pro, or Asp"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 122
- (D) OTHER INFORMATION: /note= "Xaa at position 122 is Gln, Met, Trp, Phe, Pro, His, Ile, or Tyr"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 123
- (D) OTHER INFORMATION: /note= "Xaa at position 123 is Ala, Met, Glu, Ser, or Leu"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Ala Pro Met Thr Gln Thr Thr Ser Leu Lys Thr Ser Trp Val Asn Cys
1 5 10 15

Xaa Xaa Met Ile Asp Glu Xaa Ile Xaa Xaa Leu Lys Xaa Xaa Pro Xaa
20 25 30

Pro Xaa Xaa Asp Phe Xaa Asn Leu Asn Xaa Glu Asp Xaa Xaa Ile Leu
35 40 45

Met Xaa Xaa Asn Leu Arg Xaa Xaa Asn Leu Glu Ala Phe Xaa Arg Xaa
50 55 60

Xaa Lys Xaa Xaa Xaa Asn Ala Ser Ala Ile Glu Xaa Xaa Leu Xaa Xaa
65 70 75 80

Leu Xaa Pro Cys Leu Pro Xaa Xaa Thr Ala Xaa Pro Xaa Arg Xaa Pro
85 90 95

Ile Xaa Xaa Xaa Xaa Gly Asp Trp Xaa Glu Phe Xaa Xaa Lys Leu Xaa
100 105 110

Phe Tyr Leu Xaa Xaa Leu Glu Xaa Xaa Xaa Gln Gln Thr Thr Leu
115 120 125

Ser Leu Ala Ile Phe
130

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 1
(D) OTHER INFORMATION: /note= "Met- or Met-Ala- may or may not precede the amino acid in position 1"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 3
(D) OTHER INFORMATION: /note= "Xaa at position 3 is Ser, Lys, Gly, Asp, Met, Gln, or Arg"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 4
(D) OTHER INFORMATION: /note= "Xaa at position 4 is Asn, His, Leu, Ile, Phe, Arg, or Gln"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 5
(D) OTHER INFORMATION: /note= "Xaa at position 5 is Met, Phe, Ile, Arg, Gly, Ala, or Cys"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 6
(D) OTHER INFORMATION: /note= "Xaa at position 6 is Ile, Cys, Gln, Glu, Arg, Pro, or Ala"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 7
(D) OTHER INFORMATION: /note= "Xaa at position 7 is Asp, Phe, Lys, Arg, Ala, Gly, Glu, Gln, Asn, Thr, Ser, or Val"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 8
(D) OTHER INFORMATION: /note= "Xaa at position 8 is Glu, Trp, Pro, Ser, Ala, His, Asp, Asn, Gln, Leu, Val, or Gly"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 9
(D) OTHER INFORMATION: /note= "Xaa at position 9 is Ile, Val, Ala, Leu, Gly, Trp, Lys, Phe, Ser or Arg"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 10
(D) OTHER INFORMATION: /note= "Xaa at position 10 is Ile, Gly, Val, Arg, Ser, Phe, or Leu"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 11
(D) OTHER INFORMATION: /note= "Xaa at position 11 is Thr, His, Gly, Gln, Arg, Pro, or Ala"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 12
(D) OTHER INFORMATION: /note= "Xaa at position 12 is His,
Thr, Phe, Gly, Arg, Ala, or Trp"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 13
(D) OTHER INFORMATION: /note= "Xaa at position 13 is Leu,
Gly, Arg, Thr, Ser, or Ala"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 14
(D) OTHER INFORMATION: /note= "Xaa at position 14 is Lys,
Arg, Leu, Gln, Gly, Pro, Val, or Trp"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 15
(D) OTHER INFORMATION: /note= "Xaa at position 15 is Gln,
Asn, Leu, Pro, Arg, or Val"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 16
(D) OTHER INFORMATION: /note= "Xaa at position 16 is Pro,
His, Thr, Gly, Asp, Gln, Ser, Leu, or Lys"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 17
(D) OTHER INFORMATION: /note= "Xaa at position 17 is Pro,
Asp, Gly, Ala, Arg, Leu, or Gln"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 18
(D) OTHER INFORMATION: /note= "Xaa at position 18 is Leu,
Val, Arg, Gln, Asn, Gly, Ala, or Glu"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 19
(D) OTHER INFORMATION: /note= "Xaa at position 19 is Pro,
Leu, Gln, Ala, Thr, or Glu"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 20
(D) OTHER INFORMATION: /note= "Xaa at position 20 is Leu,
Val, Gly, Ser, Lys, Glu, Gln, Thr, Arg, Ala, Phe,
Ile, or Met"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 21
(D) OTHER INFORMATION: /note= "Xaa at position 21 is Leu,
Ala, Gly, Asn, Pro, Gln, or Val"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 22
(D) OTHER INFORMATION: /note= "Xaa at position 22 is Asp,
Leu, or Val"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 23
(D) OTHER INFORMATION: /note= "Xaa at position 23 is Phe,
Ser, Pro, Trp, or Ile"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 24
(D) OTHER INFORMATION: /note= "Xaa at position 24 is Asn
or Ala"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 26
(D) OTHER INFORMATION: /note= "Xaa at position 26 is Leu,
Trp, or Arg"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 27
(D) OTHER INFORMATION: /note= "Xaa at position 27 is Asn,
Cys, Arg, Leu, His, Met, or Pro"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 28
(D) OTHER INFORMATION: /note= "Xaa at position 28 is Gly,
Asp, Ser, Cys, Ala, Lys, Asn, Thr, Leu, Val, Glu,
Phe, Tyr, Ile, or Met"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 29
(D) OTHER INFORMATION: /note= "Xaa at position 29 is Glu,
Asn, Tyr, Leu, Phe, Asp, Ala, Cys, Gln, Arg, Thr,
Gly, or Ser"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 30
(D) OTHER INFORMATION: /note= "Xaa at position 30 is Asp,
Ser, Leu, Arg, Lys, Thr, Met, Trp, Glu, Asn, Gln,
Ala, or Pro"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 31
(D) OTHER INFORMATION: /note= "Xaa at position 31 is Gln,
Pro, Phe, Val, Met, Leu, Thr, Lys, Asp, Asn, Arg,
Ser, Ala, Ile, Glu, His, or Trp"

(ix) FEATURE:
(A) NAME/KEY: Modified-site

(B) LOCATION: 32
(D) OTHER INFORMATION: /note= "Xaa at position 32 is Asp, Phe, Ser, Thr, Cys, Glu, Asn, Gln, Lys, His, Ala, Tyr, Ile, Val, or Gly"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 33
(D) OTHER INFORMATION: /note= "Xaa at position 33 is Ile, Gly, Val, Ser, Arg, Pro, or His"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 34
(D) OTHER INFORMATION: /note= "Xaa at position 34 is Leu, Ser, Cys, Arg, Ile, His, Phe, Glu, Lys, Thr, Ala, Met, Val, or Asn"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 35
(D) OTHER INFORMATION: /note= "Xaa at position 35 is Met, Arg, Ala, Gly, Pro, Asn, His, or Asp"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 36
(D) OTHER INFORMATION: /note= "Xaa at position 36 is Glu, Leu, Thr, Asp, Tyr, Lys, Asn, Ser, Ala, Ile, Val, His, Phe, Met, or Gln"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 37
(D) OTHER INFORMATION: /note= "Xaa at position 37 is Asn, Arg, Met, Pro, Ser, Thr, or His"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 38
(D) OTHER INFORMATION: /note= "Xaa at position 38 is Asn, His, Arg, Leu, Gly, Ser, or Thr"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 39
(D) OTHER INFORMATION: /note= "Xaa at position 39 is Leu, Thr, Ala, Gly, Glu, Pro, Lys, Ser, or Met"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 40
(D) OTHER INFORMATION: /note= "Xaa at position 40 is Arg, Asp, Ile, Ser, Val, Thr, Gln, Asn, Lys, His, Ala, or Leu"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 41
(D) OTHER INFORMATION: /note= "Xaa at position 41 is Arg, Thr, Val, Ser, Leu, or Gly"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 42
(D) OTHER INFORMATION: /note= "Xaa at position 42 is Pro,
Gly, Cys, Ser, Gln, Glu, Arg, His, Thr, Ala, Tyr,
Phe, Leu, Val, or Lys"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 43
(D) OTHER INFORMATION: /note= "Xaa at position 43 is Asn
or Gly"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 44
(D) OTHER INFORMATION: /note= "Xaa at position 44 is Leu,
Ser, Asp, Arg, Gln, Val, or Cys"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 45
(D) OTHER INFORMATION: /note= "Xaa at position 45 is Glu,
Tyr, His, Leu, Pro, or Arg"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 46
(D) OTHER INFORMATION: /note= "Xaa at position 46 is Ala,
Ser, Pro, Tyr, Asn, or Thr"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 47
(D) OTHER INFORMATION: /note= "Xaa at position 47 is Phe,
Asn, Glu, Pro, Lys, Arg, or Ser"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 48
(D) OTHER INFORMATION: /note= "Xaa at position 48 is Asn,
His, Val, Arg, Pro, Thr, Asp, or Ile"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 49
(D) OTHER INFORMATION: /note= "Xaa at position 49 is Arg,
Tyr, Trp, Lys, Ser, His, Pro, or Val"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 50
(D) OTHER INFORMATION: /note= "Xaa at position 50 is Ala,
Asn, Pro, Ser, or Lys"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 51
(D) OTHER INFORMATION: /note= "Xaa at position 51 is Val,
Thr, Pro, His, Leu, Phe, or Ser"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 52
(D) OTHER INFORMATION: /note= "Xaa at position 52 is Lys,
Ile, Arg, Val, Asn, Glu, or Ser"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 53
(D) OTHER INFORMATION: /note= "Xaa at position 53 is Ser,
Ala, Phe, Val, Gly, Asn, Ile, Pro, or His"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 54
(D) OTHER INFORMATION: /note= "Xaa at position 54 is Leu,
Val, Trp, Ser, Ile, Phe, Thr, or His"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 55
(D) OTHER INFORMATION: /note= "Xaa at position 55 is Gln,
Ala, Pro, Thr, Glu, Arg, Trp, Gly, or Leu"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 56
(D) OTHER INFORMATION: /note= "Xaa at position 56 is Asn,
Leu, Val, Trp, Pro, or Ala"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 57
(D) OTHER INFORMATION: /note= "Xaa at position 57 is Ala,
Met, Leu, Pro, Arg, Glu, Thr, Gln, Trp, or Asn"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 58
(D) OTHER INFORMATION: /note= "Xaa at position 58 is Ser,
Glu, Met, Ala, His, Asn, Arg, or Asp"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 59
(D) OTHER INFORMATION: /note= "Xaa at position 59 is Ala,
Glu, Asp, Leu, Ser, Gly, Thr, or Arg"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 60
(D) OTHER INFORMATION: /note= "Xaa at position 60 is Ile,
Met, Thr, Pro, Arg, Gly, Ala"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 61
(D) OTHER INFORMATION: /note= "Xaa at position 61 is
Glu, Lys, Gly, Asp, Pro, Trp, Arg, Ser, Gln,
or Leu"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 62
- (D) OTHER INFORMATION: /note= "Xaa at position 62 is Ser, Val, Ala, Asn, Trp, Glu, Pro, Gly, or Asp"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 63
- (D) OTHER INFORMATION: /note= "Xaa at position 63 is Ile, Ser, Arg, Thr, or Leu"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 64
- (D) OTHER INFORMATION: /note= "Xaa at position 64 is Leu, Ala, Ser, Glu, Phe, Gly, or Arg"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 65
- (D) OTHER INFORMATION: /note= "Xaa at position 65 is Lys, Thr, Gly, Asn, Met, Arg, Ile, or Asp"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 66
- (D) OTHER INFORMATION: /note= "Xaa at position 66 is Asn, Trp, Val, Gly, Thr, Leu, Glu, or Arg"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 67
- (D) OTHER INFORMATION: /note= "Xaa at position 67 is Leu, Gln, Gly, Ala, Trp, Arg, Val, or Lys"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 68
- (D) OTHER INFORMATION: /note= "Xaa at position 68 is Leu, Gln, Lys, Trp, Arg, Asp, Glu, Asn, His, Thr, Ser, Ala, Tyr, Phe, Ile, Met, or Val"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 69
- (D) OTHER INFORMATION: /note= "Xaa at position 69 is Pro, Ala, Thr, Trp, Arg, or Met"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 70
- (D) OTHER INFORMATION: /note= "Xaa at position 70 is Cys, Glu, Gly, Arg, Met, or Val"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 71
- (D) OTHER INFORMATION: /note= "Xaa at position 71 is Leu, Asn, Val, or Gln"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 72
(D) OTHER INFORMATION: /note= "Xaa at position 72 is Pro, Cys, Arg, Ala, or Lys"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 73
(D) OTHER INFORMATION: /note= "Xaa at position 73 is Leu, Ser, Trp, or Gly"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 74
(D) OTHER INFORMATION: /note= "Xaa at position 74 is Ala, Lys, Arg, Val, or Trp"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 75
(D) OTHER INFORMATION: /note= "Xaa at position 75 is Thr, Asp, Cys, Leu, Val, Glu, His, Asn, or Ser"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 76
(D) OTHER INFORMATION: /note= "Xaa at position 76 is Ala, Pro, Ser, Thr, Gly, Asp, Ile, or Met"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 77
(D) OTHER INFORMATION: /note= "Xaa at position 77 is Ala, Pro, Ser, Thr, Phe, Leu, Asp, or His"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 78
(D) OTHER INFORMATION: /note= "Xaa at position 78 is Pro, Phe, Arg, Ser, Lys, His, Ala, Gly, Ile, or Leu"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 79
(D) OTHER INFORMATION: /note= "Xaa at position 79 is Thr, Asp, Ser, Asn, Pro, Ala, Leu, or Arg"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 80
(D) OTHER INFORMATION: /note= "Xaa at position 80 is Arg, Ile, Ser, Glu, Leu, Val, Gln, Lys, His, Ala, or Pro"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 81
(D) OTHER INFORMATION: /note= "Xaa at position 81 is His, Gln, Pro, Arg, Val, Leu, Gly, Thr, Asn, Lys, Ser, Ala, Trp, Phe, Ile, or Tyr"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 82
(D) OTHER INFORMATION: /note= "Xaa at position 82 is Pro, Lys, Tyr, Gly, Ile, or Thr"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 83
(D) OTHER INFORMATION: /note= "Xaa at position 83 is Ile, Val, Lys, Ala, or Asn"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 84
(D) OTHER INFORMATION: /note= "Xaa at position 84 is His, Ile, Asn, Leu, Asp, Ala, Thr, Glu, Gln, Ser, Phe, Met, Val, Lys, Arg, Tyr, or Pro"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 85
(D) OTHER INFORMATION: /note= "Xaa at position 85 is Ile, Leu, Arg, Asp, Val, Pro, Gln, Gly, Ser, Phe, or His"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 86
(D) OTHER INFORMATION: /note= "Xaa at position 86 is Lys, Tyr, Leu, His, Arg, Ile, Ser, Gln, or Pro"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 87
(D) OTHER INFORMATION: /note= "Xaa at position 87 is Asp, Pro, Met, Lys, His, Thr, Val, Tyr, Glu, Asn, Ser, Ala, Gly, Ile, Leu, or Gln"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 88
(D) OTHER INFORMATION: /note= "Xaa at position 88 Gly, Leu, Glu, Lys, Ser, Tyr, or Pro"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 89
(D) OTHER INFORMATION: /note= "Xaa at position 89 is Asp or Ser"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 90
(D) OTHER INFORMATION: /note= "Xaa at position 90 is Trp, Val, Cys, Tyr, Thr, Met, Pro, Leu, Gln, Lys, Ala, Phe, or Gly"

(ix) FEATURE:
(A) NAME/KEY: Modified-site

(B) LOCATION: 91
(D) OTHER INFORMATION: /note= "Xaa at position 91 is Asn, Pro, Ala, Phe, Ser, Trp, Gln, Tyr, Leu, Lys, Ile, Asp, or His"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 92
(D) OTHER INFORMATION: /note= "Xaa at position 92 is Glu, Ser, Ala, Lys, Thr, Ile, Gly, or Pro"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 94
(D) OTHER INFORMATION: /note= "Xaa at position 94 is Arg, Lys, Asp, Leu, Thr, Ile, Gln, His, Ser, Ala, or Pro"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 95
(D) OTHER INFORMATION: /note= "Xaa at position 95 is Arg, Thr, Pro, Glu, Tyr, Leu, Ser, or Gly"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 96
(D) OTHER INFORMATION: /note= "Xaa at position 96 is Lys, Asn, Thr, Leu, Gln, Arg, His, Glu, Ser, Ala, or Trp"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 97
(D) OTHER INFORMATION: /note= "Xaa at position 97 is Leu, Ile, Arg, Asp, or Met"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 98
(D) OTHER INFORMATION: /note= "Xaa at position 98 is Thr, Val, Gln, Tyr, Glu, His, Ser, or Phe"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 99
(D) OTHER INFORMATION: /note= "Xaa at position 99 is Phe, Ser, Cys, His, Gly, Trp, Tyr, Asp, Lys, Leu, Ile, Val, or Asn"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 100
(D) OTHER INFORMATION: /note= "Xaa at position 100 is Tyr, Cys, His, Ser, Trp, Arg, or Leu"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 101
(D) OTHER INFORMATION: /note= "Xaa at position 101 is Leu, Asn, Val, Pro, Arg, Ala, His, Thr, Trp, or Met"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 102
(D) OTHER INFORMATION: /note= "Xaa at position 102 is Lys, Leu, Pro, Thr, Met, Asp, Val, Glu, Arg, Trp, Ser, Asn, His, Ala, Tyr, Phe, Gln, or Ile"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 103
(D) OTHER INFORMATION: /note= "Xaa at position 103 is Thr, Ser, Asn, Ile, Trp, Lys, or Pro"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 104
(D) OTHER INFORMATION: /note= "Xaa at position 104 is Leu, Ser, Pro, Ala, Glu, Cys, Asp, or Tyr"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 105
(D) OTHER INFORMATION: /note= "Xaa at position 105 is Glu, Ser, Lys, Pro, Leu, Thr, Tyr, or Arg"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 106
(D) OTHER INFORMATION: /note= "Xaa at position 106 is Asn, Ala, Pro, Leu, His, Val or Gln"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 107
(D) OTHER INFORMATION: /note= "Xaa at position 107 is Ala, Ser, Ile, Asn, Pro, Lys, Asp, or Gly"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 108
(D) OTHER INFORMATION: /note= "Xaa at position 108 is Gln, Ser, Met, Trp, Arg, Phe, Pro, His, Ile, Tyr, or Cys"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 109
(D) OTHER INFORMATION: /note= "Xaa at position 109 is Ala, Met, Glu, His, Ser, Pro, Tyr, or Leu"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Asn Cys Xaa
1 5 10 15

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Asn Xaa Xaa Xaa Xaa Xaa Xaa Xaa
20 25 30

Xaa
35 40 45

Xaa
50 55 60

Xaa
65 70 75 80

Xaa Phe Xaa Xaa Xaa
85 90 95

Xaa Gln Gln
100 105 110

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1
- (D) OTHER INFORMATION: /note= "Met- or Met-Ala- may or may not precede the amino acid in position 1"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 3
- (D) OTHER INFORMATION: /note= "Xaa at position 3 is Ser, Gly, Asp, Met, or Gln"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 4
- (D) OTHER INFORMATION: /note= "Xaa at position 4 is Asn, His, or Ile"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 5
- (D) OTHER INFORMATION: /note= "Xaa at position 5 is Met or Ile"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 7
- (C) OTHER INFORMATION: /note= "Xaa at position 7 is Asp or Glu"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 9
- (D) OTHER INFORMATION: /note= "Xaa at position 9 is Ile, Ala, Leu, or Gly"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 10

(D) OTHER INFORMATION: /note= "Xaa at position 10 is Ile, Val, or Leu"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 11
(D) OTHER INFORMATION: /note= "Xaa at position 11 is Thr, His, Gln, or Ala"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 12
(D) OTHER INFORMATION: /note= "Xaa at position 12 is His or Ala"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 15
(D) OTHER INFORMATION: /note= "Xaa at position 15 is Gln, Asn, or Val"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 16
(D) OTHER INFORMATION: /note= "Xaa at position 16 is Pro, Gly, or Gln"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 17
(D) OTHER INFORMATION: /note= "Xaa at position 17 is Pro, Asp, Gly, or Gln"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 18
(D) OTHER INFORMATION: /note= "Xaa at position 18 is Leu, Arg, Gln, Asn, Gly, Ala, or Glu"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 19
(D) OTHER INFORMATION: /note= "Xaa at position 19 is Pro or Glu"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 20
(D) OTHER INFORMATION: /note= "Xaa at position 20 is Leu, Val, Gly, Ser, Lys, Ala, Arg, Gln, Glu, Ile, Phe, Thr, or Met"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 21
(D) OTHER INFORMATION: /note= "Xaa at position 21 is Leu, Ala, Asn, Pro, Gln, or Val"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 23

(D) OTHER INFORMATION: /note= "Xaa at position 23 is Phe, Ser, Pro, or Trp"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 24
(D) OTHER INFORMATION: /note= "Xaa at position 24 is Asn or Ala"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 28
(D) OTHER INFORMATION: /note= "Xaa at position 28 is Gly, Asp, Ser, Cys, Ala, Asn, Ile, Leu, Met, Tyr, or Arg"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 30
(D) OTHER INFORMATION: /note= "Xaa at position 30 is Asp or Glu"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 31
(D) OTHER INFORMATION: /note= "Xaa at position 31 is Gln, Val, Met, Leu, Thr, Ala, Asn, Glu, Ser, or Lys"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 32
(D) OTHER INFORMATION: /note= "Xaa at position 32 is Asp, Phe, Ser, Thr, Ala, Asn, Gln, Glu, His, Ile, Lys, Tyr, Val, or Cys"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 36
(D) OTHER INFORMATION: /note= "Xaa at position 36 is Glu, Ala, Asn, Ser, or Asp"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 37
(D) OTHER INFORMATION: /note= "Xaa at position 37 is Asn, Arg, Met, Pro, Ser, Thr, or His"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 40
(D) OTHER INFORMATION: /note= "Xaa at position 40 is Arg or Ala"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 41
(D) OTHER INFORMATION: /note= "Xaa at position 41 is Arg, Thr, Val, Leu, or Gly"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 42

(D) OTHER INFORMATION: /note= "Xaa at position 42 is Pro, Gly, Ser, Gln, Ala, Arg, Asn, Glu, Leu, Thr, Val, or Lys"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 46
(D) OTHER INFORMATION: /note= "Xaa at position 46 is Ala or Ser"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 48
(D) OTHER INFORMATION: /note= "Xaa at position 48 is Asn, Pro, Thr, or Ile"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 49
(D) OTHER INFORMATION: /note= "Xaa at position 49 is Arg or Lys"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 50
(D) OTHER INFORMATION: /note= "Xaa at position 50 is Ala or Asn"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 51
(D) OTHER INFORMATION: /note= "Xaa at position 51 is Val or Thr"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 52
(D) OTHER INFORMATION: /note= "Xaa at position 52 is Lys or Arg"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 53
(D) OTHER INFORMATION: /note= "Xaa at position 53 is Ser, Phe, or His"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 54
(D) OTHER INFORMATION: /note= "Xaa at position 54 is Leu, Ile, Phe, or His"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 55
(D) OTHER INFORMATION: /note= "Xaa at position 55 is Gln, Ala, Pro, Thr, Glu, Arg, or Gly"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 57

(D) OTHER INFORMATION: /note= "Xaa at position 57 is Ala, Pro, or Arg"

(ix) FEATURE:

(A) NAME/KEY: Modified-site
(B) LOCATION: 58
(D) OTHER INFORMATION: /note= "Xaa at position 58 is Ser, Glu, Arg, or Asp"

(ix) FEATURE:

(A) NAME/KEY: Modified-site
(B) LOCATION: 59
(D) OTHER INFORMATION: /note= "Xaa at position 59 is Ala or Leu"

(ix) FEATURE:

(A) NAME/KEY: Modified-site
(B) LOCATION: 62
(D) OTHER INFORMATION: /note= "Xaa at position 62 is Ser, Val, Ala, Asn, Glu, Pro, or Gly"

(ix) FEATURE:

(A) NAME/KEY: Modified-site
(B) LOCATION: 63
(D) OTHER INFORMATION: /note= "Xaa at position 63 is Ile or Leu"

(ix) FEATURE:

(A) NAME/KEY: Modified-site
(B) LOCATION: 65
(D) OTHER INFORMATION: /note= "Xaa at position 65 is Lys, Thr, Gly, Asn, Met, Arg, Ile, or Asp"

(ix) FEATURE:

(A) NAME/KEY: Modified-site
(B) LOCATION: 66
(D) OTHER INFORMATION: /note= "Xaa at position 66 is Asn, Gly, Glu, or Arg"

(ix) FEATURE:

(A) NAME/KEY: Modified-site
(B) LOCATION: 68
(D) OTHER INFORMATION: /note= "Xaa at position 68 is Leu, Gln, Trp, Arg, Asp, Ala, Asn, Glu, His, Ile, Met, Phe, Ser, Thr, Tyr, or Val"

(ix) FEATURE:

(A) NAME/KEY: Modified-site
(B) LOCATION: 69
(D) OTHER INFORMATION: /note= "Xaa at position 69 is Pro or Thr"

(ix) FEATURE:

(A) NAME/KEY: Modified-site
(B) LOCATION: 71
(D) OTHER INFORMATION: /note= "Xaa at position 71 is Leu or Val"

(ix) FEATURE:

(A) NAME/KEY: Modified-site
(B) LOCATION: 73

(D) OTHER INFORMATION: /note= "Xaa at position 73 is Leu or Ser"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 74
(D) OTHER INFORMATION: /note= "Xaa at position 74 is Ala or Trp"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 77
(D) OTHER INFORMATION: /note= "Xaa at position 77 is Ala or Pro"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 79
(D) OTHER INFORMATION: /note= "Xaa at position 79 is Thr, Asp, Ser, Pro, Ala, Leu, or Arg"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 81
(D) OTHER INFORMATION: /note= "Xaa at position 81 is His, Pro, Arg, Val, Leu, Gly, Asn, Phe, Ser, or Thr"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 82
(D) OTHER INFORMATION: /note= "Xaa at position 82 is Pro or Tyr"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 83
(D) OTHER INFORMATION: /note= "Xaa at position 83 is Ile or Val"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 84
(D) OTHER INFORMATION: /note= "Xaa at position 84 is His, Ile, Asn, Leu, Ala, Thr, Arg, Gln, Lys, Met, Ser, Tyr, Val, or Pro"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 85
(D) OTHER INFORMATION: /note= "Xaa at position 85 is Ile, Leu, or Val"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 86
(D) OTHER INFORMATION: /note= "Xaa at position 86 is Lys, Arg, Ile, Gln, Pro, or Ser"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 87

(D) OTHER INFORMATION: /note= "Xaa at position 87 is Asp, Pro, Met, Lys, His, Thr, Asn, Ile, Leu, or Tyr"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 90

(D) OTHER INFORMATION: /note= "Xaa at position 90 is Trp or Leu"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 91

(D) OTHER INFORMATION: /note= "Xaa at position 91 is Asn, Pro, Ala, Ser, Trp, Gln, Tyr, Leu, Lys, Ile, Asp, or His"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 92

(D) OTHER INFORMATION: /note= "Xaa at position 92 is Glu or Gly"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 94

(C) OTHER INFORMATION: /note= "Xaa at position 94 is Arg, Ala, or Ser"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 95

(D) OTHER INFORMATION: /note= "Xaa at position 95 is Arg, Thr, Glu, Leu, or Ser"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 98

(D) OTHER INFORMATION: /note= "Xaa at position 98 is Thr, Val, or Gln"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 100

(D) OTHER INFORMATION: /note= "Xaa at position 100 is Tyr or Trp"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 101

(D) OTHER INFORMATION: /note= "Xaa at position 101 is Leu or Ala"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 102

(D) OTHER INFORMATION: /note= "Xaa at position 102 is Lys, Thr, Val, Trp, Ser, Ala, His, Met, Phe, Tyr, or Ile"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 103

(D) OTHER INFORMATION: /note= "Xaa at position 103 is Thr

or Ser"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 106
- (D) OTHER INFORMATION: /note= "Xaa at position 106 is Asn, Pro, Leu, His, Val, or Gln"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 107
- (D) OTHER INFORMATION: /note= "Xaa at position 107 is Ala, Ser, Ile, Asn, Pro, Asp, or Gly"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 108
- (D) OTHER INFORMATION: /note= "Xaa at position 108 is Gln, Ser, Met, Trp, Arg, Phe, Pro, His, Ile, Tyr, or Cys"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 109
- (D) OTHER INFORMATION: /note= "Xaa at position 109 is Ala, Met, Glu, His, Ser, Pro, Tyr, or Leu"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Asn Cys Xaa Xaa Xaa Ile Xaa Glu Xaa Xaa Xaa Xaa Leu Lys Xaa Xaa
1 5 10 15

Xaa Xaa Xaa Xaa Xaa Asp Xaa Xaa Asn Leu Asn Xaa Glu Xaa Xaa Xaa
20 25 30

Ile Leu Met Xaa Xaa Asn Leu Xaa Xaa Xaa Asn Leu Glu Xaa Phe Xaa
35 40 45

Xaa Xaa Xaa Xaa Xaa Xaa Asn Xaa Xaa Xaa Ile Glu Xaa Xaa Leu
50 55 60

Xaa Xaa Leu Xaa Xaa Cys Xaa Pro Xaa Xaa Thr Ala Xaa Pro Xaa Arg
65 70 75 80

Xaa Xaa Xaa Xaa Xaa Xaa Gly Asp Xaa Xaa Xaa Phe Xaa Xaa Lys
85 90 95

Leu Xaa Phe Xaa Xaa Xaa Xaa Leu Glu Xaa Xaa Xaa Xaa Gln Gln
100 105 110

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1
- (D) OTHER INFORMATION: /note= "Met- or Met-Ala- may or may not precede the amino acid in position 1"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 3
- (D) OTHER INFORMATION: /note= "Xaa at position 3 is Ser, Gly, Asp, or Gln"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 4
- (D) OTHER INFORMATION: /note= "Xaa at position 4 is Asn, His, or Ile"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 9
- (D) OTHER INFORMATION: /note= "Xaa at position 9 is Ile, Ala, Leu, or Gly"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 11
- (D) OTHER INFORMATION: /note= "Xaa at position 11 is Thr, His, or Gln"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 12
- (D) OTHER INFORMATION: /note= "Xaa at position 12 is His or Ala"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 15
- (D) OTHER INFORMATION: /note= "Xaa at position 15 is Gln or Asn"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 16
- (D) OTHER INFORMATION: /note= "Xaa at position 16 is Pro or Gly"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 18
- (D) OTHER INFORMATION: /note= "Xaa at position 18 is Leu, Arg, Asn, or Ala"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 20
- (D) OTHER INFORMATION: /note= "Xaa at position 20 is Leu, Val, Ser, Ala, Arg, Gln, Glu, Ile, Phe, Thr, or Met"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site

(B) LOCATION: 21
(D) OTHER INFORMATION: /note= "Xaa at position 21 is Leu, Ala, Asn, or Pro"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 24
(D) OTHER INFORMATION: /note= "Xaa at position 24 is Asn or Ala"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 28
(D) OTHER INFORMATION: /note= "Xaa at position 28 is Gly, Asp, Ser, Ala, Asn, Ile, Leu, Met, Tyr, or Arg"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 31
(D) OTHER INFORMATION: /note= "Xaa at position 31 is Gln, Val, Met, Leu, Ala, Asn, Glu, or Lys"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 32
(D) OTHER INFORMATION: /note= "Xaa at position 32 is Asp, Phe, Ser, Ala, Gln, Glu, His, Val, or Thr"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 36
(D) OTHER INFORMATION: /note= "Xaa at position 36 is Glu, Asn, Ser, or Asp"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 37
(D) OTHER INFORMATION: /note= "Xaa at position 37 is Asn, Arg, Pro, Thr, or His"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 41
(D) OTHER INFORMATION: /note= "Xaa at position 41 is Arg, Leu, or Gly"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 42
(D) OTHER INFORMATION: /note= "Xaa at position 42 is Pro, Gly, Ser, Ala, Asn, Val, Leu, or Gln"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 48
(D) OTHER INFORMATION: /note= "Xaa at position 48 is Asn, Pro, or Thr"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 50

(D) OTHER INFORMATION: /note= "Xaa at position 50 is Ala or Asn"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 51
(D) OTHER INFORMATION: /note= "Xaa at position 51 is Val or Thr"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 53
(D) OTHER INFORMATION: /note= "Xaa at position 53 is Ser or Phe"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 54
(D) OTHER INFORMATION: /note= "Xaa at position 54 is Leu or Phe"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 55
(D) OTHER INFORMATION: /note= "Xaa at position 55 is Gln, Ala, Glu, or Arg"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 62
(D) OTHER INFORMATION: /note= "Xaa at position 62 is Ser, Val, Asn, Pro, or Gly"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 63
(D) OTHER INFORMATION: /note= "Xaa at position 63 is Ile or Leu"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 65
(D) OTHER INFORMATION: /note= "Xaa at position 65 is Lys, Asn, Met, Arg, Ile, or Gly"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 66
(D) OTHER INFORMATION: /note= "Xaa at position 66 is Asn, Gly, Glu, or Arg"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 68
(D) OTHER INFORMATION: /note= "Xaa at position 68 is Leu, Gln, Trp, Arg, Asp, Asn, Glu, His, Met, Phe, Ser, Thr, Tyr, or Val"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 73

(D) OTHER INFORMATION: /note= "Xaa at position 73 is Leu or Ser"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 74
(D) OTHER INFORMATION: /note= "Xaa at position 74 is Ala or Trp"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 77
(D) OTHER INFORMATION: /note= "Xaa at position 77 is Ala or Pro"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 79
(D) OTHER INFORMATION: /note= "Xaa at position 79 is Thr, Asp, or Ala"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 81
(D) OTHER INFORMATION: /note= "Xaa at position 81 is His, Pro, Arg, Val, Gly, Asn, Ser, or Thr"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 84
(D) OTHER INFORMATION: /note= "Xaa at position 84 is His, Ile, Asn, Leu, Ala, Thr, Arg, Gln, Glu, Lys, Met, Ser, Tyr, or Val"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 85
(D) OTHER INFORMATION: /note= "Xaa at position 85 is Ile or Leu"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 86
(D) OTHER INFORMATION: /note= "Xaa at position 86 is Lys or Arg"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 87
(D) OTHER INFORMATION: /note= "Xaa at position 87 is Asp, Pro, Met, Lys, His, Pro, Asn, Ile, Leu, or Tyr"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 91
(D) OTHER INFORMATION: /note= "Xaa at position 91 is Asn, Pro, Ser, Ile, or Asp"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 94

(D) OTHER INFORMATION: /note="Xaa at position 94 is Arg, Ala, or Ser"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 95

(D) OTHER INFORMATION: /note= "Xaa at position 95 is Arg, Thr, Glu, Leu, or Ser"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 98

(D) OTHER INFORMATION: /note= "Xaa at position 98 is Thr or Gln"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 102

(D) OTHER INFORMATION: /note= "Xaa at position 102 is Lys, Val, Trp, or Ile"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 103

(D) OTHER INFORMATION: /note= "Xaa at position 103 is Thr, Ala, His, Phe, Tyr, or Ser"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 106

(D) OTHER INFORMATION: /note= "Xaa at position 106 is Asn, Pro, Leu, His, Val, or Gln"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 107

(D) OTHER INFORMATION: /note= "Xaa at position 107 is Ala, Ser, Ile, Pro, or Asp"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 108

(D) OTHER INFORMATION: /note= "Xaa at position 108 is Gln, Met, Trp, Phe, Pro, His, Ile, or Tyr"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 109

(D) OTHER INFORMATION: /note= "Xaa at position 109 is Ala, Met, Glu, Ser, or Leu"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Asn Cys Xaa Xaa Met Ile Asp Glu Xaa Ile Xaa Xaa Leu Lys Xaa Xaa
1 5 10 15

Pro Xaa Pro Xaa Xaa Asp Phe Xaa Asn Leu Asn Xaa Glu Asp Xaa Xaa
20 25 30

Ile Leu Met Xaa Xaa Asn Leu Arg Xaa Xaa Asn Leu Glu Ala Phe Xaa

35

40

45

Arg Xaa Xaa Lys Xaa Xaa Xaa Asn Ala Ser Ala Ile Glu Xaa Xaa Leu
50 55 60

Xaa Xaa Leu Xaa Pro Cys Leu Pro Xaa Xaa Thr Ala Xaa Pro Xaa Arg
65 70 75 80

Xaa Pro Ile Xaa Xaa Xaa Gly Asp Trp Xaa Glu Phe Xaa Xaa Lys
85 90 95

Leu Xaa Phe Tyr Leu Xaa Xaa Leu Glu Xaa Xaa Xaa Gln Gln
100 105 110

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 133 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1
- (D) OTHER INFORMATION: /note= "Met- may or may not precede the amino acid in position 1"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 18
- (D) OTHER INFORMATION: /note= "Xaa at position 18 is Asn or Ile"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 19
- (D) OTHER INFORMATION: /note= "Xaa at position 19 is Met, Ala, or Ile"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 20
- (D) OTHER INFORMATION: /note= "Xaa at position 20 is Ile, Pro, or Leu"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 23
- (D) OTHER INFORMATION: /note= "Xaa at position 23 is Ile, Ala, or Leu"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 25
- (D) OTHER INFORMATION: /note= "Xaa at position 25 is Thr or His"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 29
(D) OTHER INFORMATION: /note= "Xaa at position 29 is Gln,
Arg, Val, or Ile"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 32
(D) OTHER INFORMATION: /note= "Xaa at position 32 is Leu,
Ala, Asn, or Arg"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 34
(D) OTHER INFORMATION: /note= "Xaa at position 34 is Leu
or Ser"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 37
(D) OTHER INFORMATION: /note= "Xaa at position 37 is Phe,
Pro, or Ser"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 38
(D) OTHER INFORMATION: /note= "Xaa at position 38 is Asn
or Ala"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 42
(D) OTHER INFORMATION: /note= "Xaa at position 42 is Gly,
Ala, Ser, Asp, or Asn"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 45
(D) OTHER INFORMATION: /note= "Xaa at position 45 is Gln,
Val, or Met"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 46
(D) OTHER INFORMATION: /note= "Xaa at position 46 is Asp
or Ser"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 49
(D) OTHER INFORMATION: /note= "Xaa at position 49 is Met,
Ile, Leu, or Asp"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 50
(D) OTHER INFORMATION: /note= "Xaa at position 50 is Glu
or Asp"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 51

(D) OTHER INFORMATION: /note= "Xaa at position 51 is Asn, Arg, or Ser"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 55
(D) OTHER INFORMATION: /note= "Xaa at position 55 is Arg, Leu, or Thr"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 56
(D) OTHER INFORMATION: /note= "Xaa at position 56 is Pro or Ser"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 59
(D) OTHER INFORMATION: /note= "Xaa at position 59 is Glu or Leu"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 60
(D) OTHER INFORMATION: /note= "Xaa at position 60 is Ala or Ser"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 62
(D) OTHER INFORMATION: /note= "Xaa at position 62 is Asn Val, or Pro"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 63
(D) OTHER INFORMATION: /note= "Xaa at position 63 is Arg or His"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 65
(D) OTHER INFORMATION: /note= "Xaa at position 65 is Val or Ser"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 67
(D) OTHER INFORMATION: /note= "Xaa at position 67 is Ser, Asn, His, or Gln"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 69
(D) OTHER INFORMATION: /note= "Xaa at position 69 is Gln or Glu"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 73
(D) OTHER INFORMATION: /note= "Xaa at position 73 is Ala

or Gly"

- (ix) FEATURE:
 - (A) NAME/KEY: Modified-site
 - (B) LOCATION: 76
 - (D) OTHER INFORMATION: /note= "Xaa at position 76 is Ser, Ala, or Pro"
- (ix) FEATURE:
 - (A) NAME/KEY: Modified-site
 - (B) LOCATION: 79
 - (D) OTHER INFORMATION: /note= "Xaa at position 79 is Lys, Arg, or Ser"
- (ix) FEATURE:
 - (A) NAME/KEY: Modified-site
 - (B) LOCATION: 82
 - (D) OTHER INFORMATION: /note= "Xaa at position 82 is Leu, Glu, Val, or Trp"
- (ix) FEATURE:
 - (A) NAME/KEY: Modified-site
 - (B) LOCATION: 85
 - (D) OTHER INFORMATION: /note= "Xaa at position 85 is Leu or Val"
- (ix) FEATURE:
 - (A) NAME/KEY: Modified-site
 - (B) LOCATION: 87
 - (D) OTHER INFORMATION: /note= "Xaa at position 87 is Leu, Ser, or Tyr"
- (ix) FEATURE:
 - (A) NAME/KEY: Modified-site
 - (B) LOCATION: 88
 - (D) OTHER INFORMATION: /note= "Xaa at position 88 is Ala or Trp"
- (ix) FEATURE:
 - (A) NAME/KEY: Modified-site
 - (B) LOCATION: 91
 - (D) OTHER INFORMATION: /note= "Xaa at position 91 is Ala or Pro"
- (ix) FEATURE:
 - (A) NAME/KEY: Modified-site
 - (B) LOCATION: 93
 - (D) OTHER INFORMATION: /note= "Xaa at position 93 is Pro or Ser"
- (ix) FEATURE:
 - (A) NAME/KEY: Modified-site
 - (B) LOCATION: 95
 - (D) OTHER INFORMATION: /note= "Xaa at position 95 is His or Thr"
- (ix) FEATURE:
 - (A) NAME/KEY: Modified-site
 - (B) LOCATION: 98
 - (D) OTHER INFORMATION: /note= "Xaa at position 98 is His, Ile, or Thr"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 100
(D) OTHER INFORMATION: /note= "Xaa at position 100 is Lys or Arg"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 101
(D) OTHER INFORMATION: /note= "Xaa at position 101 is Asp, Ala, or Met"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 105
(D) OTHER INFORMATION: /note= "Xaa at position 105 is Asn or Glu"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 109
(D) OTHER INFORMATION: /note= "Xaa at position 109 is Arg, Glu, or Leu"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 112
(D) OTHER INFORMATION: /note= "Xaa at position 112 is Thr or Gln"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 116
(D) OTHER INFORMATION: /note= "Xaa at position 116 is Lys, Val, Trp, or Ser"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 117
(D) OTHER INFORMATION: /note= "Xaa at position 117 is Thr or Ser"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 120
(D) OTHER INFORMATION: /note= "Xaa at position 120 is Asn, Gln, or His"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 123
(D) OTHER INFORMATION: /note= "Xaa at position 123 is Ala or Glu"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Ala Pro Met Thr Gln Thr Thr Ser Leu Lys Thr Ser Trp Val Asn Cys
1 5 10 15

Ser Xaa Xaa Xaa Asp Glu Xaa Ile Xaa His Leu Lys Xaa Pro Pro Xaa
20 25 30

Pro Xaa Leu Asp Xaa Xaa Asn Leu Asn Xaa Glu Asp Xaa Xaa Ile Leu
 35 40 45

Xaa Xaa Xaa Asn Leu Arg Xaa Xaa Asn Leu Xaa Xaa Phe Xaa Xaa Ala
 50 55 60

Xaa Lys Xaa Leu Xaa Asn Ala Ser Xaa Ile Glu Xaa Ile Leu Xaa Asn
 65 70 75 80

Leu Xaa Pro Cys Xaa Pro Xaa Xaa Thr Ala Xaa Pro Xaa Arg Xaa Pro
 85 90 95

Ile Xaa Ile Xaa Xaa Gly Asp Trp Xaa Glu Phe Arg Xaa Lys Leu Xaa
 100 105 110

Phe Tyr Leu Xaa Xaa Leu Glu Xaa Ala Gln Xaa Gln Gln Thr Thr Leu
 115 120 125

Ser Leu Ala Ile Phe
 130

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 111 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: Modified-site
 - (B) LOCATION: 1
 - (D) OTHER INFORMATION: /note= "Met- or Met-Ala may or may not precede the amino acid in position 1"
- (ix) FEATURE:
 - (A) NAME/KEY: Modified-site
 - (B) LOCATION: 4
 - (D) OTHER INFORMATION: /note= "Xaa at position 4 is Asn or Ile"
- (ix) FEATURE:
 - (A) NAME/KEY: Modified-site
 - (B) LOCATION: 5
 - (D) OTHER INFORMATION: /note= "Xaa at position 5 is Met, Ala, or Ile"
- (ix) FEATURE:
 - (A) NAME/KEY: Modified-site
 - (B) LOCATION: 6
 - (D) OTHER INFORMATION: /note= "Xaa at position 6 is Ile, Pro, or Leu"
- (ix) FEATURE:
 - (A) NAME/KEY: Modified-site
 - (B) LOCATION: 9
 - (D) OTHER INFORMATION: /note= "Xaa at position 9 is Ile, Ala, or Leu"

(ix) FEATURE:
(A) NAM/KEY: Modified-site
(B) LOCATION: 11
(D) OTHER INFORMATION: /note= "Xaa at position 11 is Thr or His"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 15
(D) OTHER INFORMATION: /note= "Xaa at position 15 is Gln, Arg, Val, or Ile"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 18
(D) OTHER INFORMATION: /note= "Xaa at position 18 is Leu, Ala, Asn, or Arg"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 20
(D) OTHER INFORMATION: /note= "Xaa at position 20 is Leu or Ser"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 23
(D) OTHER INFORMATION: /note= "Xaa at position 23 is Phe, Pro, or Ser"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 24
(D) OTHER INFORMATION: /note= "Xaa at position 24 is Asn or Ala"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 28
(D) OTHER INFORMATION: /note= "Xaa at position 28 is Gly, Ala, Ser, Asp, or Asn"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 31
(D) OTHER INFORMATION: /note= "Xaa at position 31 is Gln, Val, or Met"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 32
(D) OTHER INFORMATION: /note= "Xaa at position 32 is Asp or Ser"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 35
(D) OTHER INFORMATION: /note= "Xaa at position 35 is Met, Ile, or Asp"

(ix) FEATURE:

(A) NAME/KEY: Modified-site
(B) LOCATION 36
(D) OTHER INFORMATION: /note= "Xaa at position 36 is Glu or Asp"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 37
(D) OTHER INFORMATION: /note= "Xaa at position 37 is Asn, Arg, or Ser"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 41
(D) OTHER INFORMATION: /note= "Xaa at position 41 is Arg, Leu, or Thr"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION 42
(D) OTHER INFORMATION: /note= "Xaa at position 42 is Pro or Ser"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 45
(D) OTHER INFORMATION: /note= "Xaa at position 45 is Glu or Leu"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 46
(D) OTHER INFORMATION: /note= "Xaa at position 46 is Ala or Ser"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 48
(D) OTHER INFORMATION: /note= "Xaa at position 48 is Asn, Val, or Pro"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 49
(D) OTHER INFORMATION: /note= "Xaa at position 49 is Arg or His"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 51
(D) OTHER INFORMATION: /note= "Xaa at position 51 is Val or Ser"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 53
(D) OTHER INFORMATION: /note= "Xaa at position 53 is Ser, Asn, His, or Gln"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 55
(D) OTHER INFORMATION: /note= "Xaa at position 55 is Gln"

or Glu"

- (ix) FEATURE:
 - (A) NAME/KEY: Modified-site
 - (B) LOCATION: 59
 - (D) OTHER INFORMATION: /note= "Xaa at position 59 is Ala or Gly"

- (ix) FEATURE:
 - (A) NAME/KEY: Modified-site
 - (B) LOCATION: 62
 - (D) OTHER INFORMATION: /note= "Xaa at position 62 is Ser, Ala, or Pro"

- (ix) FEATURE:
 - (A) NAME/KEY: Modified-site
 - (B) LOCATION: 65
 - (D) OTHER INFORMATION: /note= "Xaa at position 65 is Lys, Arg, or Ser"

- (ix) FEATURE:
 - (A) NAME/KEY: Modified-site
 - (B) LOCATION: 67
 - (D) OTHER INFORMATION: /note= "Xaa at position 67 is Leu, Glu, or Val"

- (ix) FEATURE:
 - (A) NAME/KEY: Modified-site
 - (B) LOCATION: 68
 - (D) OTHER INFORMATION: /note= "Xaa at position 68 is Leu, Glu, Val, or Trp"

- (ix) FEATURE:
 - (A) NAME/KEY: Modified-site
 - (B) LOCATION: 71
 - (D) OTHER INFORMATION: /note= "Xaa at position 71 is Leu or Val"

- (ix) FEATURE:
 - (A) NAME/KEY: Modified-site
 - (B) LOCATION: 73
 - (D) OTHER INFORMATION: /note= "Xaa at position 73 is Leu, Ser, or Tyr"

- (ix) FEATURE:
 - (A) NAME/KEY: Modified-site
 - (B) LOCATION: 74
 - (D) OTHER INFORMATION: /note= "Xaa at position 74 is Ala or Trp"

- (ix) FEATURE:
 - (A) NAME/KEY: Modified-site
 - (B) LOCATION: 77
 - (D) OTHER INFORMATION: /note= "Xaa at position 77 is Ala or Pro"

- (ix) FEATURE:
 - (A) NAME/KEY: Modified-site
 - (B) LOCATION: 79
 - (D) OTHER INFORMATION: /note= "Xaa at position 79 is Pro or Ser"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 81
(D) OTHER INFORMATION: /note= "Xaa at position 81 is His or Thr"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 84
(D) OTHER INFORMATION: /note= "Xaa at position 84 is His, Ile, or Thr"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 86
(D) OTHER INFORMATION: /note= "Xaa at position 86 is Lys or Arg"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 87
(D) OTHER INFORMATION: /note= "Xaa at position 87 is Asp, Ala, or Met"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 91
(D) OTHER INFORMATION: /note= "Xaa at position 91 is Asn or Glu"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 95
(D) OTHER INFORMATION: /note= "Xaa at position 95 is Arg, Glu, or Leu"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 98
(D) OTHER INFORMATION: /note= "Xaa at position 98 is Thr or Gln"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 102
(D) OTHER INFORMATION: /note= "Xaa at position 102 is Lys, Val, Trp, or Ser"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 103
(D) OTHER INFORMATION: /note= "Xaa at position 103 is Thr or Ser"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 106
(D) OTHER INFORMATION: /note= "Xaa at position 106 is Asn, Gln, or His"

(ix) FEATURE:
(A) NAME/KEY: Modified-site

(B) LOCATION: 109

(D) OTHER INFORMATION: /note= "Xaa at position 109 is Ala
or Glu"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Asn	Cys	Ser	Xaa	Xaa	Xaa	Asp	Glu	Xaa	Ile	Xaa	His	Leu	Lys	Xaa	Pro
1															15
			5												
Pro	Xaa	Pro	Xaa	Leu	Asp	Xaa	Xaa	Asn	Leu	Asn	Xaa	Glu	Asp	Xaa	Xaa
				20											30
Ile	Leu	Xaa	Xaa	Xaa	Asn	Leu	Arg	Xaa	Xaa	Asn	Leu	Xaa	Xaa	Phe	Xaa
					35										45
Xaa	Ala	Xaa	Lys	Xaa	Leu	Xaa	Asn	Ala	Ser	Xaa	Ile	Glu	Xaa	Ile	Leu
					50										60
Xaa	Asn	Xaa	Xaa	Pro	Cys	Xaa	Pro	Xaa	Xaa	Thr	Ala	Xaa	Pro	Xaa	Arg
				65						75					80
Xaa	Pro	Ile	Xaa	Ile	Xaa	Xaa	Gly	Asp	Trp	Xaa	Glu	Phe	Arg	Xaa	Lys
					85				90						95
Leu	Xaa	Phe	Tyr	Leu	Xaa	Xaa	Leu	Glu	Xaa	Ala	Gln	Xaa	Gln	Gln	
					100				105						110

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Asn	Cys	Ser	Ile	Met	Ile	Asp	Glu	Ile	Ile	His	His	Leu	Lys	Arg	Pro
1															15
Pro	Ala	Pro	Leu	Leu	Asp	Pro	Asn	Asn	Leu	Asn	Ala	Glu	Asp	Val	Asp
				20											30
Ile	Leu	Met	Glu	Asn	Asn	Leu	Arg	Arg	Pro	Asn	Leu	Glu	Ala	Phe	Asn
					35										45
Arg	Ala	Val	Lys	Ser	Leu	Gln	Asn	Ala	Ser	Ala	Ile	Glu	Ser	Ile	Leu
					50										60
Lys	Asn	Leu	Leu	Pro	Cys	Leu	Pro	Leu	Ala	Thr	Ala	Ala	Pro	Thr	Arg
				65						75					80
His	Pro	Ile	His	Ile	Lys	Asp	Gly	Asp	Trp	Asn	Glu	Phe	Arg	Arg	Lys
					85				90						95
Leu	Thr	Phe	Tyr	Leu	Lys	Thr	Leu	Glu	Asn	Ala	Gln	Ala	Gln	Gln	
					100				105						110

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 amino acids
- (B) TYPE: amino acid
- (C) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Asn	Cys	Ser	Ile	Met	Ile	Asp	Glu	Ile	Ile	His	His	Leu	Lys	Arg	Pro
1					5				10					15	
Pro	Asn	Pro	Leu	Leu	Asp	Pro	Asn	Asn	Leu	Asn	Ser	Glu	Asp	Met	Asp
			20					25					30		
Ile	Leu	Met	Glu	Asn	Asn	Leu	Arg	Arg	Pro	Asn	Leu	Glu	Ala	Phe	Asn
		35				40						45			
Arg	Ala	Val	Lys	Ser	Leu	Gln	Asn	Ala	Ser	Ala	Ile	Glu	Ser	Ile	Leu
		50			55				60						
Lys	Asn	Leu	Leu	Pro	Cys	Leu	Pro	Leu	Ala	Thr	Ala	Ala	Pro	Thr	Arg
		65			70			75					80		
His	Pro	Ile	His	Ile	Lys	Asp	Gly	Asp	Trp	Asn	Glu	Phe	Arg	Arg	Lys
			85			90						95			
Leu	Thr	Phe	Tyr	Leu	Lys	Thr	Leu	Glu	Asn	Ala	Gln	Ala	Gln		
		100					105					110			

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 amino acids
- (B) TYPE: amino acid
- (C) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Asn	Cys	Ser	Ile	Met	Ile	Asp	Glu	Ile	Ile	His	His	Leu	Lys	Val	Pro
1					5				10					15	
Pro	Ala	Pro	Leu	Leu	Asp	Ser	Asn	Asn	Leu	Asn	Ser	Glu	Asp	Met	Asp
			20					25					30		
Ile	Leu	Met	Glu	Asn	Asn	Leu	Arg	Arg	Pro	Asn	Leu	Glu	Ala	Phe	Asn
		35				40						45			
Arg	Ala	Val	Lys	Ser	Leu	Gln	Asn	Ala	Ser	Ala	Ile	Glu	Ser	Ile	Leu
		50			55				60						
Lys	Asn	Leu	Leu	Pro	Cys	Leu	Pro	Leu	Ala	Thr	Ala	Ala	Pro	Thr	Arg

65

70

75

80

His Pro Ile His Ile Lys Asp Gly Asp Trp Asn Glu Phe Arg Arg Lys
85 90 95

Leu Thr Phe Tyr Leu Lys Thr Leu Glu Asn Ala Gln Ala Gln Gln
100 105 110

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 amino acids
- (B) TYPE: amino acid
- (C) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Asn Cys Ser Asn Met Ile Asp Glu Ile Ile Thr His Leu Lys Gln Pro
1 5 10 15

Pro Leu Pro Leu Leu Asp Phe Asn Asn Leu Asn Gly Glu Asp Gln Asp
20 25 30

Ile Leu Met Glu Arg Asn Leu Arg Leu Pro Asn Leu Leu Ala Phe Val
35 40 45

Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Ala Ile Glu Ser Ile Leu
50 55 60

Lys Asn Leu Leu Pro Cys Leu Pro Leu Ala Thr Ala Ala Pro Thr Arg
65 70 75 80

His Pro Ile His Ile Lys Asp Gly Asp Trp Asn Glu Phe Arg Arg Lys
85 90 95

Leu Thr Phe Tyr Leu Lys Thr Leu Glu Asn Ala Gln Ala Gln Gln
100 105 110

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 amino acids
- (B) TYPE: amino acid
- (C) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Asn Cys Ser Asn Met Ile Asp Glu Ile Ile Thr His Leu Lys Gln Pro
1 5 10 15

Pro Leu Pro Leu Leu Asp Phe Asn Asn Leu Asn Gly Glu Asp Gln Asp
20 25 30

Ile Leu Met Glu Arg Asn Leu Arg Leu Pro Asn Leu Glu Ser Phe Val
35 40 45

Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Ala Ile Glu Ser Ile Leu
50 55 60

Lys Asn Leu Leu Pro Cys Leu Pro Leu Ala Thr Ala Ala Pro Thr Arg
65 70 75 80

His Pro Ile His Ile Lys Asp Gly Asp Trp Asn Glu Phe Arg Arg Lys
85 90 95

Leu Thr Phe Tyr Leu Lys Thr Leu Glu Asn Ala Gln Ala Gln Gln
100 105 110

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Asn Cys Ser Asn Met Ile Asp Glu Ile Ile Thr His Leu Lys Gln Pro
1 5 10 15

Pro Leu Pro Leu Leu Asp Phe Asn Asn Leu Asn Gly Glu Asp Gln Asp
20 25 30

Ile Leu Met Glu Arg Asn Leu Arg Thr Pro Asn Leu Leu Ala Phe Val
35 40 45

Arg Ala Val Lys His Leu Glu Asn Ala Ser Ala Ile Glu Ser Ile Leu
50 55 60

Lys Asn Leu Leu Pro Cys Leu Pro Leu Ala Thr Ala Ala Pro Thr Arg
65 70 75 80

His Pro Ile His Ile Lys Asp Gly Asp Trp Asn Glu Phe Arg Arg Lys
85 90 95

Leu Thr Phe Tyr Leu Lys Thr Leu Glu Asn Ala Gln Ala Gln Gln
100 105 110

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Asn	Cys	Ser	Asn	Met	Ile	Asp	Glu	Ile	Ile	Thr	His	Leu	Lys	Gln	Pro
1				5					10					15	
Pro	Leu	Pro	Leu	Leu	Asp	Phe	Asn	Asn	Leu	Asn	Gly	Glu	Asp	Gln	Asp
				20				25					30		
Ile	Leu	Met	Glu	Asn	Asn	Leu	Arg	Arg	Pro	Asn	Leu	Glu	Ala	Phe	Asn
				35				40					45		
Arg	Ala	Val	Lys	Ser	Leu	Gln	Asn	Ala	Ser	Gly	Ile	Glu	Ala	Ile	Leu
				50				55				60			
Arg	Asn	Leu	Gln	Pro	Cys	Leu	Pro	Ser	Ala	Thr	Ala	Ala	Pro	Ser	Arg
				65				70					80		
His	Pro	Ile	Ile	Ile	Lys	Ala	Gly	Asp	Trp	Gln	Glu	Phe	Arg	Arg	Lys
					85				90				95		
Leu	Thr	Phe	Tyr	Leu	Lys	Thr	Leu	Glu	Asn	Ala	Gln	Ala	Gln	Gln	
				100				105					110		

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 111 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Asn	Cys	Ser	Asn	Met	Ile	Asp	Glu	Ile	Ile	Thr	His	Leu	Lys	Gln	Pro
1				5					10					15	
Pro	Leu	Pro	Leu	Leu	Asp	Phe	Asn	Asn	Leu	Asn	Gly	Glu	Asp	Gln	Asp
				20				25					30		
Ile	Leu	Met	Glu	Asn	Asn	Leu	Arg	Arg	Pro	Asn	Leu	Glu	Ala	Phe	Asn
				35				40					45		
Arg	Ala	Val	Lys	Ser	Leu	Gln	Asn	Ala	Ser	Gly	Ile	Glu	Ala	Ile	Leu
				50				55				60			
Arg	Asn	Leu	Val	Pro	Cys	Leu	Pro	Ser	Ala	Thr	Ala	Ala	Pro	Ser	Arg
				65				70					80		
His	Pro	Ile	Thr	Ile	Lys	Ala	Gly	Asp	Trp	Gln	Glu	Phe	Arg	Arg	Lys
					85				90				95		
Leu	Thr	Phe	Tyr	Leu	Lys	Thr	Leu	Glu	Asn	Ala	Gln	Ala	Gln	Gln	
				100				105					110		

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 111 amino acids
 - (B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Asn Cys Ser Asn Met Ile Asp Glu Ile Ile Thr His Leu Lys Gln Pro
1 5 10 15
Pro Leu Pro Leu Leu Asp Phe Asn Asn Leu Asn Gly Glu Asp Gln Asp
20 25 30
Ile Leu Met Glu Asn Asn Leu Arg Arg Pro Asn Leu Glu Ala Phe Asn
35 40 45
Arg Ala Val Lys Ser Leu Gln Asn Ala Ser Ala Ile Glu Ser Ile Leu
50 55 60
Lys Asn Leu Leu Pro Cys Leu Pro Leu Ala Thr Ala Ala Pro Thr Arg
65 70 75 80
His Pro Ile His Ile Lys Asp Gly Asp Trp Asn Glu Phe Arg Glu Lys
85 90 95
Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu Gln Gln
100 105 110

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 amino acids
- (B) TYPE: amino acid
- (C) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Asn Cys Ser Asn Met Ile Asp Glu Ile Ile Thr His Leu Lys Gln Pro
1 5 10 15
Pro Leu Pro Leu Leu Asp Phe Asn Asn Leu Asn Gly Glu Asp Gln Asp
20 25 30
Ile Leu Met Glu Asn Asn Leu Arg Arg Pro Asn Leu Glu Ala Phe Asn
35 40 45
Arg Ala Val Lys Ser Leu Gln Asn Ala Ser Ala Ile Glu Ser Ile Leu
50 55 60
Lys Asn Leu Leu Pro Cys Leu Pro Leu Ala Thr Ala Ala Pro Thr Arg
65 70 75 80
His Pro Ile His Ile Lys Asp Gly Asp Trp Asn Glu Phe Arg Glu Lys
85 90 95
Leu Thr Phe Tyr Leu Val Ser Leu Glu His Ala Gln Glu Gln Gln

100

105

110

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 amino acids
- (B) TYPE: amino acid
- (C) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Asn	Cys	Ser	Asn	Met	Ile	Asp	Glu	Ile	Ile	Thr	His	Leu	Lys	Gln	Pro
1				5					10						15
Pro	Leu	Pro	Leu	Leu	Asp	Phe	Asn	Asn	Leu	Asn	Gly	Glu	Asp	Gln	Asp
	20							25						30	
Ile	Leu	Met	Glu	Asn	Asn	Leu	Arg	Arg	Pro	Asn	Leu	Glu	Ala	Phe	Asn
	35						40						45		
Arg	Ala	Val	Lys	Ser	Leu	Gln	Asn	Ala	Ser	Gly	Ile	Glu	Ala	Ile	Leu
	50						55				60				
Arg	Asn	Leu	Gln	Pro	Cys	Leu	Pro	Ser	Ala	Thr	Ala	Ala	Pro	Ser	Arg
	65				70				75					80	
His	Pro	Ile	Ile	Ile	Lys	Ala	Gly	Asp	Trp	Gln	Glu	Phe	Arg	Glu	Lys
		85						90					95		
Leu	Thr	Phe	Tyr	Leu	Val	Thr	Leu	Glu	Gln	Ala	Gln	Glu	Gln	Gln	
		100						105					110		

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 amino acids
- (B) TYPE: amino acid
- (C) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Asn	Cys	Ser	Asn	Met	Ile	Asp	Glu	Ile	Ile	Thr	His	Leu	Lys	Gln	Pro
1				5					10						15
Pro	Leu	Pro	Leu	Leu	Asp	Phe	Asn	Asn	Leu	Asn	Gly	Glu	Asp	Gln	Asp
	20							25					30		
Ile	Leu	Met	Glu	Asn	Asn	Leu	Arg	Arg	Pro	Asn	Leu	Glu	Ala	Phe	Asn
	35						40					45			
Arg	Ala	Val	Lys	Ser	Leu	Gln	Asn	Ala	Ser	Gly	Ile	Glu	Ala	Ile	Leu
	50						55				60				

Arg	Asn	Leu	Val	Pro	Cys	Leu	Pro	Ser	Ala	Thr	Ala	Ala	Pro	Ser	Arg
65						70				75				80	
His	Pro	Ile	Thr	Ile	Lys	Ala	Gly	Asp	Trp	Gln	Glu	Phe	Arg	Glu	Lys
								85		90				95	
Leu	Thr	Phe	Tyr	Leu	Val	Thr	Leu	Glu	Gln	Ala	Gln	Glu	Gln	Gln	
						100			105			110			

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Asn	Cys	Ser	Asn	Met	Ile	Asp	Glu	Ile	Ile	Thr	His	Leu	Lys	Gln	Pro
1					5				10				15		
Pro	Leu	Pro	Leu	Leu	Asp	Phe	Asn	Asn	Leu	Asn	Gly	Glu	Asp	Gln	Asp
					20				25			30			
Ile	Leu	Met	Glu	Asn	Asn	Leu	Arg	Arg	Pro	Asn	Leu	Glu	Ala	Phe	Asn
					35				40			45			
Arg	Ala	Val	Lys	Ser	Leu	Gln	Asn	Ala	Ser	Gly	Ile	Glu	Ala	Ile	Leu
					50			55			60				
Arg	Asn	Leu	Val	Pro	Cys	Leu	Pro	Ser	Ala	Thr	Ala	Ala	Pro	Ser	Arg
65						70				75			80		
His	Pro	Ile	Thr	Ile	Lys	Ala	Gly	Asp	Trp	Gln	Glu	Phe	Arg	Glu	Lys
						85			90			95			
Leu	Thr	Phe	Tyr	Leu	Val	Ser	Leu	Glu	His	Ala	Gln	Glu	Gln	Gln	
						100			105			110			

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

Asn	Cys	Ser	Ile	Met	Ile	Asp	Glu	Ile	Ile	His	His	Leu	Lys	Arg	Pro
1						5			10				15		
Pro	Ala	Pro	Leu	Leu	Asp	Pro	Asn	Asn	Leu	Asn	Ala	Glu	Asp	Val	Asp
					20				25			30			

Ile Leu Met Glu Arg Asn Leu Arg Leu Pro Asn Leu Glu Ser Phe Val
35 40 45
Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Ala Ile Glu Ser Ile Leu
50 55 60
Lys Asn Leu Leu Pro Cys Leu Pro Leu Ala Thr Ala Ala Pro Thr Arg
65 70 75 80
His Pro Ile His Ile Lys Asp Gly Asp Trp Asn Glu Phe Arg Arg Lys
85 90 95
Leu Thr Phe Tyr Leu Lys Thr Leu Glu Asn Ala Gln Ala Gln Gln
100 105 110

(2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 111 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys Arg Pro
1 5 10 15
Pro Asn Pro Leu Leu Asp Pro Asn Asn Leu Asn Ser Glu Asp Met Asp
20 25 30
Ile Leu Met Glu Arg Asn Leu Arg Thr Pro Asn Leu Leu Ala Phe Val
35 40 45
Arg Ala Val Lys His Leu Glu Asn Ala Ser Ala Ile Glu Ser Ile Leu
50 55 60
Lys Asn Leu Leu Pro Cys Leu Pro Leu Ala Thr Ala Ala Pro Thr Arg
65 70 75 80
His Pro Ile His Ile Lys Asp Gly Asp Trp Asn Glu Phe Arg Arg Lys
85 90 95
Leu Thr Phe Tyr Leu Lys Thr Leu Glu Asn Ala Gln Ala Gln Gln
100 105 110

(2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 111 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

Asn	Cys	Ser	Ile	Met	Ile	Asp	Glu	Ile	Ile	His	His	Leu	Lys	Val	Pro
1				5					10						15
Pro	Ala	Pro	Leu	Leu	Asp	Ser	Asn	Asn	Leu	Asn	Ser	Glu	Asp	Met	Asp
			20						25					30	
Ile	Leu	Met	Glu	Arg	Asn	Leu	Arg	Leu	Pro	Asn	Leu	Leu	Ala	Phe	Val
		35					40						45		
Arg	Ala	Val	Lys	Asn	Leu	Glu	Asn	Ala	Ser	Ala	Ile	Glu	Ser	Ile	Leu
		50			55						60				
Lys	Asn	Leu	Leu	Pro	Cys	Leu	Pro	Leu	Ala	Thr	Ala	Ala	Pro	Thr	Arg
		65			70				75					80	
His	Pro	Ile	His	Ile	Lys	Asp	Gly	Asp	Trp	Asn	Glu	Phe	Arg	Arg	Lys
			85				90						95		
Leu	Thr	Phe	Tyr	Leu	Lys	Thr	Leu	Glu	Asn	Ala	Gln	Ala	Gln	Gln	
			100				105						110		

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (C) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

Met	Ala	Asn	Cys	Ser	Asn	Met	Ile	Asp	Glu	Ile	Ile	Thr	His	Leu	Lys
1						5			10				15		
Gln	Pro	Pro	Leu	Pro	Leu	Leu	Asp	Phe	Asn	Asn	Leu	Asn	Gly	Glu	Asp
			20				25						30		
Gln	Asp	Ile	Leu	Met	Glu	Asn	Asn	Leu	Arg	Arg	Pro	Asn	Leu	Glu	Ala
		35				40				45					
Phe	Asn	Arg	Ala	Val	Lys	Ser	Leu	Gln	Asn	Ala	Ser	Gly	Ile	Glu	Ala
		50			55			60							
Ile	Leu	Arg	Asn	Leu	Gln	Pro	Cys	Leu	Pro	Ser	Ala	Thr	Ala	Ala	Pro
		65				70		75					80		
Ser	Arg	His	Pro	Ile	Ile	Lys	Ala	Gly	Asp	Trp	Gln	Glu	Phe	Arg	
			85				90					95			
Glu	Lys	Leu	Thr	Phe	Tyr	Leu	Val	Thr	Leu	Glu	Gln	Ala	Gln	Glu	Gln
			100				105					110			
Gln															

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 113 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

Met	Ala	Asn	Cys	Ser	Asn	Met	Ile	Asp	Glu	Ile	Ile	Thr	His	Leu	Lys
1															15
Gln	Pro	Pro	Leu	Pro	Leu	Leu	Asp	Phe	Asn	Asn	Leu	Asn	Gly	Glu	Asp
															30
Gln	Asp	Ile	Leu	Met	Glu	Asn	Asn	Leu	Arg	Arg	Pro	Asn	Leu	Glu	Ala
															45
Phe	Asn	Arg	Ala	Val	Lys	Ser	Leu	Gln	Asn	Ala	Ser	Gly	Ile	Glu	Ala
															60
Ile	Leu	Arg	Asn	Leu	Val	Pro	Cys	Leu	Pro	Ser	Ala	Thr	Ala	Ala	Pro
															80
Ser	Arg	His	Pro	Ile	Thr	Ile	Lys	Ala	Gly	Asp	Trp	Gln	Glu	Phe	Arg
															95
Glu	Lys	Leu	Thr	Phe	Tyr	Leu	Val	Thr	Leu	Glu	Gln	Ala	Gln	Glu	Gln
															110
Gln															

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 113 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

Met	Ala	Asn	Cys	Ser	Asn	Met	Ile	Asp	Glu	Ile	Ile	Thr	His	Leu	Lys
1															15
Gln	Pro	Pro	Leu	Pro	Leu	Leu	Asp	Phe	Asn	Asn	Leu	Asn	Gly	Glu	Asp
															30
Gln	Asp	Ile	Leu	Met	Glu	Asn	Asn	Leu	Arg	Arg	Pro	Asn	Leu	Glu	Ala
															45
Phe	Asn	Arg	Ala	Val	Lys	Ser	Leu	Gln	Asn	Ala	Ser	Gly	Ile	Glu	Ala
															60

Ile Leu Arg Asn Leu Val Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro
65 70 75 80

Ser Arg His Pro Ile Thr Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg
85 90 95

Glu Lys Leu Thr Phe Tyr Leu Val Ser Leu Glu His Ala Gln Glu Gln
100 105 110

Gln

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys
1 5 10 15

Arg Pro Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn Ala Glu Asp
20 25 30

Val Asp Ile Leu Met Glu Arg Asn Leu Arg Leu Pro Asn Leu Glu Ser
35 40 45

Phe Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Ala Ile Glu Ser
50 55 60

Ile Leu Lys Asn Leu Leu Pro Cys Leu Pro Leu Ala Thr Ala Ala Pro
65 70 75 80

Thr Arg His Pro Ile His Ile Lys Asp Gly Asp Trp Asn Glu Phe Arg
85 90 95

Arg Lys Leu Thr Phe Tyr Leu Lys Thr Leu Glu Asn Ala Gln Ala Gln
100 105 110

Gln

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys
 1 5 10 15

Arg Pro Pro Asn Pro Leu Leu Asp Pro Asn Asn Leu Asn Ser Glu Asp
 20 25 30

Met Asp Ile Leu Met Glu Arg Asn Leu Arg Thr Pro Asn Leu Leu Ala
 35 40 45

Phe Val Arg Ala Val Lys His Leu Glu Asn Ala Ser Ala Ile Glu Ser
 50 55 60

Ile Leu Lys Asn Leu Leu Pro Cys Leu Pro Leu Ala Thr Ala Ala Pro
 65 70 75 80

Thr Arg His Pro Ile His Ile Lys Asp Gly Asp Trp Asn Glu Phe Arg
 85 90 95

Arg Lys Leu Thr Phe Tyr Leu Lys Thr Leu Glu Asn Ala Gln Ala Gln
 100 105 110

Gln

(2) INFORMATION FOR SEQ ID NO:30:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 113 amino acids
 - (B) TYPE: amino acid
 - (C) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys
 1 5 10 15

Val Pro Pro Ala Pro Leu Leu Asp Ser Asn Asn Leu Asn Ser Glu Asp
 20 25 30

Met Asp Ile Leu Met Glu Arg Asn Leu Arg Leu Pro Asn Leu Ala
 35 40 45

Phe Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Ala Ile Glu Ser
 50 55 60

Ile Leu Lys Asn Leu Leu Pro Cys Leu Pro Leu Ala Thr Ala Ala Pro
 65 70 75 80

Thr Arg His Pro Ile His Ile Lys Asp Gly Asp Trp Asn Glu Phe Arg
 85 90 95

Arg Lys Leu Thr Phe Tyr Leu Lys Thr Leu Glu Asn Ala Gln Ala Gln
 100 105 110

Gln

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

```

Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys
1          5          10          15

Arg Pro Pro Asn Pro Leu Leu Asp Pro Asn Asn Leu Asn Ser Glu Asp
20          25          30

Met Asp Ile Leu Met Glu Arg Asn Leu Arg Thr Pro Asn Leu Leu Ala
35          40          45

Phe Val Arg Ala Val Lys His Leu Glu Asn Ala Ser Gly Ile Glu Ala

```

50

55

60

Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro
65 70 75 80

Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg
85 90 95

Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu Gln
100 105 110

Gln

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys
1 5 10 15

Val Pro Pro Ala Pro Leu Leu Asp Ser Asn Asn Leu Asn Ser Glu Asp
20 25 30

Met Asp Ile Leu Met Glu Arg Asn Leu Arg Leu Pro Asn Leu Leu Ala
35 40 45

Phe Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Gly Ile Glu Ala
50 55 60

Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro
65 70 75 80

Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg
85 90 95

Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu Gln
100 105 110

Gln

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys
1 5 10 15

Arg Pro Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn Ala Glu Asp
20 25 30

Val Asp Ile Leu Met Glu Arg Asn Leu Arg Leu Pro Asn Leu Glu Ser
35 40 45

Phe Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Gly Ile Glu Ala
50 55 60

Ile Leu Arg Asn Leu Val Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro
65 70 75 80

Ser Arg His Pro Ile Thr Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg
85 90 95

Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu Gln
100 105 110

Gln

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (C) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys
1 5 10 15

Val Pro Pro Ala Pro Leu Leu Asp Ser Asn Asn Leu Asn Ser Glu Asp
20 25 30

Met Asp Ile Leu Met Glu Arg Asn Leu Arg Leu Pro Asn Leu Leu Ala
35 40 45

Phe Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Gly Ile Glu Ala
50 55 60

Ile Leu Arg Asn Leu Val Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro
65 70 75 80

Ser Arg His Pro Ile Thr Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg
85 90 95

Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu Gln
100 105 110

Gln

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys
1 5 10 15

Arg Pro Pro Asn Pro Leu Leu Asp Pro Asn Asn Leu Asn Ser Glu Asp
20 25 30

Met Asp Ile Leu Met Glu Arg Asn Leu Arg Thr Pro Asn Leu Leu Ala
35 40 45

Phe Val Arg Ala Val Lys His Leu Glu Asn Ala Ser Gly Ile Glu Ala
50 55 60

Ile Leu Arg Asn Leu Val Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro
65 70 75 80

Ser Arg His Pro Ile Thr Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg
85 90 95

Glu Lys Leu Thr Phe Tyr Leu Val Ser Leu Glu His Ala Gln Glu Gln
100 105 110

Gln

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys
1 5 10 15

Val Pro Pro Ala Pro Leu Leu Asp Ser Asn Asn Leu Asn Ser Glu Asp
20 25 30

Met Asp Ile Leu Met Glu Arg Asn Leu Arg Leu Pro Asn Leu Leu Ala
35 40 45

Phe Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Gly Ile Glu Ala
50 55 60

Ile Leu Arg Asn Leu Val Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro
65 70 75 80

Ser Arg His Pro Ile Thr Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg
85 90 95

Glu Lys Leu Thr Phe Tyr Leu Val Ser Leu Glu His Ala Gln Glu Gln
100 105 110

Gln

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys
1 5 10 15

Arg Pro Pro Asn Pro Leu Leu Asp Pro Asn Asn Leu Asn Ser Glu Asp
20 25 30

Met Asp Ile Leu Met Glu Arg Asn Leu Arg Thr Pro Asn Leu Leu Ala
35 40 45

Phe Val Arg Ala Val Lys His Leu Glu Asn Ala Ser Gly Ile Glu Ala
50 55 60

Ile Leu Arg Asn Leu Val Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro
65 70 75 80

Ser Arg His Pro Ile Thr Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg
85 90 95

Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu Gln
100 105 110

Gln

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys
1 5 10 15

Arg Pro Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn Ala Glu Asp
20 25 30

Val Asp Ile Leu Met Glu Arg Asn Leu Arg Leu Pro Asn Leu Glu Ser
35 40 45

Phe Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Gly Ile Glu Ala
50 55 60

Ile Leu Arg Asn Leu Val Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro
65 70 75 80

Ser Arg His Pro Ile Thr Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg
85 90 95

Glu Lys Leu Thr Phe Tyr Leu Val Ser Leu Glu His Ala Gln Glu Gln
100 105 110

Gln

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (C) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys
1 5 10 15

Arg Pro Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn Ala Glu Asp
20 25 30

Val Asp Ile Leu Met Asp Arg Asn Leu Arg Leu Ser Asn Leu Glu Ser
35 40 45

Phe Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Gly Ile Glu Ala
50 55 60

Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro
65 70 75 80

Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg
85 90 95

Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu Gln

100

105

110

Gln

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

Met	Ala	Asn	Cys	Ser	Ile	Met	Ile	Asp	Glu	Ala	Ile	His	His	Leu	Lys
1						5			10					15	
Arg	Pro	Pro	Ala	Pro	Ser	Leu	Asp	Pro	Asn	Asn	Leu	Asn	Asp	Glu	Asp
						20		25					30		
Met	Ser	Ile	Leu	Met	Glu	Arg	Asn	Leu	Arg	Leu	Pro	Asn	Leu	Glu	Ser
					35		40					45			
Phe	Val	Arg	Ala	Val	Lys	Asn	Leu	Glu	Asn	Ala	Ser	Gly	Ile	Glu	Ala
					50		55			60					
Ile	Leu	Arg	Asn	Leu	Gln	Pro	Cys	Leu	Pro	Ser	Ala	Thr	Ala	Ala	Pro
					65		70		75				80		
Ser	Arg	His	Pro	Ile	Ile	Ile	Lys	Ala	Gly	Asp	Trp	Gln	Glu	Phe	Arg
					85		90					95			
Glu	Lys	Leu	Thr	Phe	Tyr	Leu	Val	Thr	Leu	Glu	Gln	Ala	Gln	Glu	Gln
					100			105				110			

Gln

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

Met	Ala	Asn	Cys	Ser	Ile	Met	Ile	Asp	Glu	Ile	Ile	His	His	Leu	Lys
1						5			10				15		
Arg	Pro	Pro	Ala	Pro	Leu	Leu	Asp	Pro	Asn	Asn	Leu	Asn	Asp	Glu	Asp
					20			25				30			

Met Ser Ile Leu Met Glu Arg Asn Leu Arg Leu Pro Asn Leu Glu Ser			
35	40	45	
Phe Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Gly Ile Glu Ala			
50	55	60	
Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro			
65	70	75	80
Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg			
85	90	95	
Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu Gln			
100	105	110	
Gln			

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 113 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys
1 5 10 15

Arg Pro Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn Asp Glu Asp
20 25 30

Val Ser Ile Leu Met Glu Arg Asn Leu Arg Leu Pro Asn Leu Glu Ser
35 40 45

Phe Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Gly Ile Glu Ala
50 55 60

Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro
65 70 75 80

Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg
85 90 95

Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu Gln
100 105 110

Gln

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (C) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys
1 5 10 15

Arg Pro Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn Asp Glu Asp
20 25 30

Met Ser Ile Leu Met Glu Arg Asn Leu Arg Leu Pro Asn Leu Glu Ser
35 40 45

Phe Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Gly Ile Glu Ala
50 55 60

Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro
65 70 75 80

Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg
85 90 95

Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu Gln
100 105 110

Gln

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 125 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

Met Ala Tyr Pro Glu Thr Asp Tyr Lys Asp Asp Asp Asp Lys Asn Cys
1 5 10 15

Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys Arg Pro Pro Ala
20 25 30

Pro Leu Leu Asp Pro Asn Asn Leu Asn Ala Glu Asp Val Asp Ile Leu
35 40 45

Met Glu Arg Asn Leu Arg Leu Pro Asn Leu Glu Ser Phe Val Arg Ala
50 55 60

Val Lys Asn Leu Glu Asn Ala Ser Gly Ile Glu Ala Ile Leu Arg Asn
65 70 75 80

Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro Ser Arg His Pro
85 90 95

Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg Glu Lys Leu Thr
100 105 110

Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu Gln Gln
115 120 125

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 125 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

Met Ala Tyr Pro Glu Thr Asp Tyr Lys Asp Asp Asp Asp Lys Asn Cys
1 5 10 15

Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys Arg Pro Pro Asn

20

25

30

Pro	Leu	Leu	Asp	Pro	Asn	Asn	Leu	Asn	Ser	Glu	Asp	Met	Asp	Ile	Leu
35							40					45			
Met	Glu	Arg	Asn	Leu	Arg	Thr	Pro	Asn	Leu	Leu	Ala	Phe	Val	Arg	Ala
50						55					60				
Val	Lys	His	Leu	Glu	Asn	Ala	Ser	Gly	Ile	Glu	Ala	Ile	Leu	Arg	Asn
65						70				75		80			
Leu	Gln	Pro	Cys	Leu	Pro	Ser	Ala	Thr	Ala	Ala	Pro	Ser	Arg	His	Pro
						85				90		95			
Ile	Ile	Ile	Lys	Ala	Gly	Asp	Trp	Gln	Glu	Phe	Arg	Glu	Lys	Leu	Thr
						100		105				110			
Phe	Tyr	Leu	Val	Thr	Leu	Glu	Gln	Ala	Gln	Glu	Gln	Gln			
						115		120			125				

(2) INFORMATION FOR SEQ ID NO:48:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 113 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

Met	Ala	Asn	Cys	Ser	Ile	Met	Ile	Asp	Glu	Leu	Ile	His	His	Leu	Lys
1						5			10			15			
Ile	Pro	Pro	Asn	Pro	Ser	Leu	Asp	Ser	Ala	Asn	Leu	Asn	Ser	Glu	Asp
						20		25			30				
Val	Ser	Ile	Leu	Met	Glu	Arg	Asn	Leu	Arg	Thr	Pro	Asn	Leu	Leu	Ala
						35		40			45				
Phe	Val	Arg	Ala	Val	Lys	His	Leu	Glu	Asn	Ala	Ser	Gly	Ile	Glu	Ala
						50		55			60				
Ile	Leu	Arg	Asn	Leu	Gln	Pro	Cys	Leu	Pro	Ser	Ala	Thr	Ala	Ala	Pro
						65		70		75		80			
Ser	Arg	His	Pro	Ile	Ile	Lys	Ala	Gly	Asp	Trp	Gln	Glu	Phe	Arg	
						85		90			95				
Glu	Lys	Leu	Thr	Phe	Tyr	Leu	Val	Thr	Leu	Glu	Gln	Ala	Gln	Glu	Gln
						100		105			110				
Gln															

(2) INFORMATION FOR SEQ ID NO:49:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 134 amino acids

(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

Met Ala Pro Met Thr Gln Thr Thr Ser Leu Lys Thr Ser Trp Val Asn
1 5 10 15

Cys Ser Asn Met Ile Asp Glu Ile Ile Thr His Leu Lys Gln Pro Pro
20 25 30

Leu Pro Leu Leu Asp Phe Asn Asn Leu Asn Gly Glu Asp Gln Asp Ile
35 40 45

Leu Met Glu Asn Asn Leu Arg Arg Pro Asn Leu Glu Ala Phe Asn Arg
50 55 60

Ala Val Lys Ser Leu Gln Asn Ala Ser Ala Ile Glu Ser Ile Leu Lys
65 70 75 80

Asn Leu Leu Pro Cys Leu Pro Leu Ala Thr Ala Ala Pro Thr Arg His
85 90 95

Pro Ile His Ile Lys Asp Gly Asp Trp Asn Glu Phe Arg Arg Lys Leu
100 105 110

Thr Phe Tyr Leu Lys Thr Leu Glu Asn Ala Gln Ala Gln Gln Thr Thr
115 120 125

Leu Ser Leu Ala Ile Phe
130

(2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 36 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

Gly Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly Ser Gly Gly Gly
1 5 10 15

Ser Glu Gly Gly Ser Glu Gly Gly Ser Glu Gly Gly Gly Ser
20 25 30

Gly Gly Gly Ser
35

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

Ile	Ser	Glu	Pro	Ser	Gly	Pro	Ile	Ser	Thr	Ile	Asn	Pro	Ser	Pro	Pro
1				5					10						15
Ser Lys Glu Ser His Lys Ser Pro															
20															

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

Ile	Glu	Gly	Arg	Ile	Ser	Glu	Pro	Ser	Gly	Pro	Ile	Ser	Thr	Ile	Asn
1				5					10						15
Pro Ser Pro Pro Ser Lys Glu Ser His Lys Ser Pro															
20															
25															

(2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 906 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

ATGGCTAACT	GCTCTATAAT	GATCGATGAA	ATTATACATC	ACTTAAAGAG	ACCACCTAAC	60
CCTTTGCTGG	ACCCGAACAA	CCTCAATTCT	GAAGACATGG	ATATCCTGAT	GGAACGAAAC	120
CTTCGAACTC	CAAACCTGCT	CGCATTGTA	AGGGCTGTCA	AGCACTTAGA	AAATGCATCA	180
GGTATTGAGG	CAATTCTTCG	TAATCTCAA	CCATGTCTGC	CCTCTGCCAC	GGCCGCACCC	240

TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG	300
TTCTATCTGG TTACCCCTTGA GCAAGCGCAG GAACAACAGT ACGTAATCGA GGGAAAGGATT	360
TCCCCGGGTG GTGGTTCTGG CGGCGGCTCC AACATGGCTA CACCATTAGG CCCTGCCAGC	420
TCCCTGCCCC AGAGCTTCCT GCTCAAGTGC TTAGAGCAAG TGAGGAAGAT CCAGGGCGAT	480
GGCGCAGCGC TCCAGGAGAA GCTGTGTGCC ACCTACAAGC TGTGCCACCC CGAGGGAGCTG	540
TGCTGCTCG GACACTCTCT GGGCATCCCC TGGGCTCCCC TGAGCTCCTG CCCCAGCCAG	600
GCCCTGCAGC TGGCAGGCTG CTTGAGCAA CTCCATAGCG GCCTTTCTGC CTACCAGGGG	660
CTCCTGCAGG CCCTGGAAGG GATATCCCCC GAGTTGGTC CCACCTTGGA CACACTGCAG	720
CTGGACGTG CCGACTTTGC CACCACCATC TAACTGGAA TGGCCCTG CCGTGCAGCCC	780
ACCCAGGGTG CCATGCCGGC CTTCGCCTCT GCTTCCAGC GCCGGGCAGG AGGGGTCTG	840
GTTGCTAGCC ATCTGCAGAG CTTCTGGAG GTGTCGTACC GCGTTCTACG CCACCTTGC	900
CAGCCC	906

(2) INFORMATION FOR SEQ ID NO:54:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 732 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTAAC	60
CCTTGCTGG ACCCGAACAA CCTCAATTCT GAAGACATGG ATATCCTGAT GGAACGAAAC	120
CTTCGAACTC CAAACCTGCT CGCATTGTA AGGGCTGTCA AGCACTTAGA AAATGCATCA	180
GGTATTGAGG CAATTCTCG TAATCTCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC	240
TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG	300
TTCTATCTGG TTACCCCTTGA GCAAGCGCAG GAACAACAGT ACGTAATCGA GGGAAAGGATT	360
TCCCCGGGTG GTGGTTCTGG CGGCGGCTCC AACATGGCTA ACTGCTCTAT AATGATCGAT	420
GAAATTATAC ATCACTTAAA GAGACCACCT AACCCCTTGC TGGACCCGAA CAACCTCAAT	480
TCTGAAGACA TGGATATCCT GATGGAACGA AACCTTCGAA CTCCAAACCT GCTCGCATT	540
GTAAGGGCTG TCAAGCACTT AGAAAATGCA TCAGGTATTG AGGCAATTCT TCGTAATCTC	600
CAACCATGTC TGCCCTCTGC CACGGCCGCA CCCTCTCGAC ATCCAATCAT CATCAAGGCA	660

GGTGA CAGGAAC	ACTGGC ATTCCG AAAACTG TTCTATC TGGTAC ACAAC AG	720 732
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(2) INFORMATION FOR SEQ ID NO:55:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 777 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTAAC	60
CCTTGCTGG ACCCGAACAA CCTCAATTCT GAAGACATGG ATATCCTGAT GGAACGAAAC	120
CTTCGAACTC CAAACCTGCT CGCATTGTA AGGGCTGTCA AGCACTTAGA AAATGCATCA	180
GGTATTGAGG CAATTCTCG TAATCTCAA CCATGTCTGC CCTCTGCCAC GGCGCACCC	240
TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG	300
TTCTATCTGG TTACCCCTGA GCAAGCGCAG GAACAACAGT ACGTAATCGA GGGAAAGGATT	360
TCCCCGGGTG GTGGTTCTGG CGGCGGCTCC AACATGGCAC CGGCTCGTTC CCCGTCCCCG	420
TCTACCCAGC CGTGGGAACA CGTGAATGCC ATCCAGGAGG CCCGGCGTCT CCTGAACCTG	480
AGTAGAGACA CTGCTGCTGA GATGAATGAA ACAGTAGAAG TGATATCAGA AATGTTTGAC	540
CTCCAGGAGC CGACTTGCCT ACAGACCCGC CTGGAGCTGT ACAAGCAGGG CCTGCGGGGC	600
AGCCTCACCA AGCTCAAGGG CCCCTTGACC ATGATGGCCA GCCACTACAA GCAGCACTGC	660
CCTCCAACCC CGGAAACTTC CTGTGCAACC CAGATTATCA CCTTTGAAAG TTTCAAAGAG	720
AACCTGAAGG ACTTCCTGCT TGTCATCCCC TTTGACTGCT GGGAGCCAGT CCAGGAG	777

(2) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 921 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTAAC	60
CCTTTGCTGG ACCCGAACAA CCTCAATTCT GAAGACATGG ATATCCTGAT GGAACGAAAC	120
CTTCGAACTC CAAACCTGCT CGCATTGTA AGGGCTGTCA AGCACTTAGA AAATGCATCA	180
GGTATTGAGG CAATTCTCG TAATCTCAA CCATGTCTGC CCTCTGCCAC GGCGCACCC	240
TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG	300
TTCTATCTGG TTACCCCTTGA GCAAGCGCAG GAACAACAGT ACGTAATCGA GGGAGGATT	360
TCCCCGGGTG GTGGTTCTGG CGGCGGCTCC AACATGGCTA CACCATTGGG CCCTGCCAGC	420
TCCCTGCCCT AGAGCTTCCT GCTCAAGTCT TTAGAGCAAG TGAGGAAGAT CCAGGGCGAT	480
GGCGCAGCGC TCCAGGAGAA GCTGTGTGCC ACCTACAAGC TGTGCCACCC CGAGGAGCTG	540
GTGCTGCTCG GACACTCTCT GGGCATCCCC TGGGCTCCCC TGAGCTCCTG CCCCAGCCAG	600
GCCCTGCAGC TGGCAGGCTG CTTGAGCAA CTCCATAGCG GCCTTTCCCT CTACCAGGGG	660
CTCCTGCAGG CCCTGGAAGG GATATCCCC GAGTTGGTC CCACCTTGGA CACACTGCAG	720
CTGGACGTCTG CCGACTTTGC CACCACCATC TGGCAGCAGA TGGAAGAACT GGGAAATGGCC	780
CCTGCCCTGC AGCCCACCCA GGGTGCATG CCGGCCTTCG CCTCTGCTTT CCAGCGCCGG	840
GCAGGAGGGG TCCTGGTTGC TAGCCATCTG CAGAGCTTCC TGGAGGTGTC GTACCGCGTT	900
CTACGCCACC TTGCGCAGCC C	921

(2) INFORMATION FOR SEQ ID NO:57:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 951 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTAAC	60
CCTTTGCTGG ACCCGAACAA CCTCAATTCT GAAGACATGG ATATCCTGAT GGAACGAAAC	120
CTTCGAACTC CAAACCTGCT CGCATTGTA AGGGCTGTCA AGCACTTAGA AAATGCATCA	180
GGTATTGAGG CAATTCTCG TAATCTCAA CCATGTCTGC CCTCTGCCAC GGCGCACCC	240
TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG	300
TTCTATCTGG TTACCCCTTGA GCAAGCGCAG GAACAACAGT ACGTAATCGA GGGAGGATT	360
TCCCCGGGTG GTGGTTCTGG CGGCGGCTCC AACATGGCTC CAGTACCACC AGGTGAAGAT	420

TCCAAAGATG TGGCCGCCCG ACACAGACAG CCACACACCT CTTCAGAACG AATTGACAAA	480
CAAATTGGT ACATCCTCGA CGGGATATCA GCCCTGAGAA AGGAGACATG TAACAAGAGT	540
AACATGTGTG AAAGCAGCAA AGAGGCGCTA GCAGAAAACA ACCTGAACCT TCCAAAGATG	600
GCTGAAAAAG ATGGATGCTT CCAATCCGGA TTCAATGAGG AGACTTGCTT GGTGAAAATC	660
ATCACTGGTC TTTTGGAGTT TGAGGTATAC CTCGAGTACC TCCAGAACAG ATTTGAGAGT	720
AGTGAGGAAC AAGCCAGAGC TGTGCAGATG TCGACAAAAG TCCTGATCCA GTTCCCTGCAG	780
AAAAAGGCAA AGAATCTAGA TGCAATAACC ACCCCTGACC CAACCACAAA TGCATCCCTG	840
CTGACGAAGC TGCAGGCACA GAACCAGTGG CTGCAGGACA TGACAACCTCA TCTCATTCTG	900
CGCAGCTTTA AGGAGTTCT GCAGTCCAGC CTGAGGGCTC TTCGGCAAAT G	951

(2) INFORMATION FOR SEQ ID NO:58:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 732 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

ATGGCTTAAC GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTAAC	60
CCTTTGCTGG ACCCGAACAA CCTCAATTCT GAAGACATGG ATATCCTGAT GGAACGAAAC	120
CTTCGAACTC CAAACCTGCT CGCATTGTA AGGGCTGTCA AGCACTTAGA AAATGCATCA	180
GGTATTGAGG CAATTCTTCG TAATCTCAA CCATGTCTGC CCTCTGCCAC GGCGCACCC	240
TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG	300
TTCTATCTGG TTACCCCTGA GCAAGCGCAG GAACAACAGT ACGTAATCGA GGGAAAGATT	360
TCCCCGGGTG GTGGTTCTGG CGGGGGCTCC AACATGGCTA ACTGCTCTAT AATGATCGAT	420
GAAATTATAC ATCACTTAAA GAGACCACCT AACCCCTTGC TGGACCCGAA CAACCTCAAT	480
TCTGAAGACA TGGATATCCT GATGGAACGA AACCTTCGAA CTCCAAACCT GCTCGCATT	540
GTAAGGGCTG TCAAGCACTT AGAAAATGCA TCAGGTATTG AGGCAATTCT TCGTAATCTC	600
CAACCATGTC TGCCCTCTGC CACGGCCGCA CCCTCTCGAC ATCCAATCAT CATCAAGGCA	660
GGTGAATGGC AAGAATTCCG GGAAAAACTG ACGTTCTATC TGGTTACCCCT TGAGCAAGCG	720
CAGGAACAAAC AG	732

(2) INFORMATION FOR SEQ ID NO:59:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 921 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTAAC	60
CCTTTGCTGG ACCCGAACAA CCTCAATTCT GAAGACATGG ATATCCTGAT GGAACGAAAC	120
CTTCGAACTC CAAACCTGCT CGCATTGTA AGGGCTGTCA AGCACTTAGA AAATGCATCA	180
GGTATTGAGG CAATTCTTCG TAATCTCAA CCATGTCTGC CCTCTGCCAC GGCGCACCC	240
TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG	300
TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAGT ACGTAATCGA GGGAAAGATT	360
TCCCCGGGTG GTGGTTCTGG CGGCGGCTCC AACATGGCTA CACCATTGGG CCCTGCCAGC	420
TCCCTGCCCC AGAGCTTCCT GCTCAAGTCT TTAGAGCAAG TGAGGAAGAT CCAGGGCGAT	480
GGCGCAGCGC TCCAGGAGAA GCTGTGTGCC ACCTACAAGC TGTGCCACCC CGAGGAGCTG	540
GTGCTGCTCG GACACTCTCT GGGCATCCCC TGGGCTCCCC TGAGCTCCTG CCCCAGCCAG	600
GCCCTGCAGC TGGCAGGCTG CTTGAGCAA CTCCATAGCG GCCTTTCT GCCTACAGGGG	660
CTCCTGCAGG CCCTGGAAGG GATATCCCCC GAGTTGGTC CCACCTTGGA CACACTGCAG	720
CTGGACGTCTG CCGACTTTGC CACCACCATC TGGCAGCAGA TGGAAGAACT GGGAAATGGCC	780
CCTGCCCTGC AGCCCCACCA GGGTGCCATG CCGGCCTTCG CCTCTGCTTT CCAGCGCCGG	840
GCAGGAGGGG TCCTGGTTGC TAGCCATCTG CAGAGCTTCC TGGAGGTGTC GTACCGCGTT	900
CTACGCCACC TTGCGCAGCC C	921

(2) INFORMATION FOR SEQ ID NO:60:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 921 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTAAC	60
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CCTTTGCTGG	ACCCGAACAA	CCTCAATTCT	GAAGACATGG	ATATCCTGAT	GGAACGAAAC	120
CTTCGAACTC	CAAACCTGCT	CGCATTGTA	AGGGCTGTCA	AGCACTTAGA	AAATGCATCA	180
GGTATTGAGG	CAATTCTCG	TAATCTCAA	CCATGTCTGC	CCTCTGCCAC	GGCCGCACCC	240
TCTCGACATC	CAATCATCAT	CAAGGCAGGT	GACTGGCAAG	AATTCCGGGA	AAAAC TGACG	300
TTCTATCTGG	TTACCCCTGGA	GCAAGCGCAG	GAACAACAGT	ACGTAGAGGG	CGGTGGAGGC	360
TCCCCGGGTG	GTGGTTCTGG	CGGCGGCTCC	AACATGGCTA	CACCATTGGG	CCCTGCCAGC	420
TCCCTGCC	AGAGCTTCCT	GCTCAAGTCT	TTAGAGCAAG	TGAGGAAGAT	CCAGGGCGAT	480
GGCGCAGCGC	TCCAGGAGAA	GCTGTGTGCC	ACCTACAAGC	TGTGCCACCC	CGAGGAGCTG	540
GTGCTGCTCG	GACACTCTCT	GGGCATCCCC	TGGGCTCCCC	TGAGCTCCTG	CCCCAGCCAG	600
GCCCTGCAGC	TGGCAGGCTG	CTTGAGCCAA	CTCCATAGCG	GCCTTTCCCT	CTACCAGGGG	660
CTCCTGCAGG	CCCTGGAAGG	GATATCCCC	GAGTTGGTC	CCACCTTGG	CACACTGCAG	720
CTGGACGTG	CCGACTTTGC	CACCACCATC	TGGCAGCAGA	TGGAAGAACT	GGGAATGGCC	780
CCTGCCCTGC	AGCCCACCCA	GGGTGCCATG	CCGGCCTCG	CCTCTGCTTT	CCAGCGCCGG	840
GCAGGAGGGG	TCCTGGTTGC	TAGCCATCTG	CAGAGCTTCC	TGGAGGTGTC	GTACCGCGTT	900
CTACGCCACC	TTGCGCAGCC	C				921

(2) INFORMATION FOR SEQ ID NO:61:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 732 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

ATGGCTAACT	GCTCTATAAT	GATCGATGAA	ATTATACATC	ACTTAAAGAG	ACCACCTAAC	60
CCTTTGCTGG	ACCCGAACAA	CCTCAATTCT	GAAGACATGG	ATATCCTGAT	GGAACGAAAC	120
CTTCGAACTC	CAAACCTGCT	CGCATTGTA	AGGGCTGTCA	AGCACTTAGA	AAATGCATCA	180
GGTATTGAGG	CAATTCTCG	TAATCTCAA	CCATGTCTGC	CCTCTGCCAC	GGCCGCACCC	240
TCTCGACATC	CAATCATCAT	CAAGGCAGGT	GACTGGCAAG	AATTCCGGGA	AAAAC TGACG	300
TTCTATCTGG	TTACCCCTGGA	GCAAGCGCAG	GAACAACAGT	ACGTAGAGGG	CGGTGGAGGC	360
TCCCCGGGTG	GTGGTTCTGG	CGGCGGCTCC	AACATGGCTA	ACTGCTCTAT	AATGATCGAT	420
GAAATTATAC	ATCACTTAAA	GAGACCACCT	AACCTTTGC	TGGACCCGAA	CAACCTCAAT	480

TCTGAAGACA TGGATATCCT GATGGAACGA AACCTTCGAA CTCCAAACCT GCTCGCATTC	540
GTAAGGGCTG TCAAGCACTT AGAAAATGCA TCAGGTATTG AGGCAATTCT TCGTAATCTC	600
CAACCATGTC TGCCCTCTGC CACGGCCGCA CCCTCTCGAC ATCCAATCAT CATCAAGGCA	660
GGTGACTGGC AAGAATTCCG GGAAAAACTG ACGTTCTATC TGGTTACCCCT TGAGCAAGCG	720
CAGGAACAAAC AG	732

(2) INFORMATION FOR SEQ ID NO:62:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 777 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

ATGGCTTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTAAC	60
CCTTTGCTGG ACCCGAACAA CCTCAATTCT GAAGACATGG ATATCCTGAT GGAACGAAAC	120
CTTCGAACTC CAAACCTGCT CGCATTGTA AGGGCTGTCA AGCACTTAGA AAATGCATCA	180
GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCGCACCC	240
TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG	300
TTCTATCTGG TTACCCCTGA GCAAGCGCAG GAACAACAGT ACGTAATCGA GGGAGGATT	360
TCCCCGGGTG AACCGTCTGG TCCAATCTCT ACTATCAACC CGTCTCCTCC GTCTAAAGAA	420
TCTCATAAAAT CTCCAAACAT GGCTAACTGC TCTATAATGA TCGATGAAAT TATACATCAC	480
TTAAAGAGAC CACCTAACCC TTTGCTGGAC CCGAACAAACC TCAATTCTGA AGACATGGAT	540
ATCCTGATGG AACGAAACCT TCGAACTCCA AACCTGCTCG CATTGTAAG GGCTGTCAAG	600
CACTTAGAAA ATGCATCAGG TATTGAGGCA ATTCTTCGTA ATCTCCAACC ATGTCTGCC	660
TCTGCCACGG CCGCACCCCTC TCGACATCCA ATCATCATCA AGGCAGGTGA CTGGCAAGAA	720
TTCCGGGAAA AACTGACGTT CTATCTGGTT ACCCTTGAGC AAGCGCAGGA ACAACAG	777

(2) INFORMATION FOR SEQ ID NO:63:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 777 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTAAC	60
CCTTTGCTGG ACCCGAACAA CCTCAATTCT GAAGACATGG ATATCCTGAT GGAACGAAAC	120
CTTCGAACTC CAAACCTGCT CGCATTGTA AGGGCTGTCA AGCACTTAGA AAATGCATCA	180
GGTATTGAGG CAATTCTCG TAATCTCAA CCATGTCTGC CCTCTGCCAC GGCGCACCC	240
TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG	300
TTCTATCTGG TTACCCCTGGA GCAAGCGCAG GAACAACAGT ACGTAATCGA GGGAAAGATT	360
TCCCCGGGTG AACCGTCTGG TCCAATCTCT ACTATCAACC CGTCTCCTCC GTCTAAAGAA	420
TCTCATAAAAT CTCCAAACAT GGCTAACTGC TCTATAATGA TCGATGAAAT TATACATCAC	480
TTAAAGAGAC CACCTAACCC TTTGCTGGAC CCGAACAAACC TCAATTCTGA AGACATGGAT	540
ATCCTGATGG AACGAAACCT TCGAACTCCA AACCTGCTCG CATTGTAAG GGCTGTCAAG	600
CACTTAGAAA ATGCATCAGG TATTGAGGCA ATTCTCGTA ATCTCCAACC ATGTCTGCC	660
TCTGCCACGG CCGCACCCCTC TCGACATCCA ATCATCATCA AGGCAGGTGA CTGGCAAGAA	720
TTCCGGGAAA AACTGACGTT CTATCTGGTT ACCCTTGAGC AAGCGCAGGA ACAACAG	777

(2) INFORMATION FOR SEQ ID NO:64:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 777 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTAAC	60
CCTTTGCTGG ACCCGAACAA CCTCAATTCT GAAGACATGG ATATCCTGAT GGAACGAAAC	120
CTTCGAACTC CAAACCTGCT CGCATTGTA AGGGCTGTCA AGCACTTAGA AAATGCATCA	180
GGTATTGAGG CAATTCTCG TAATCTCAA CCATGTCTGC CCTCTGCCAC GGCGCACCC	240
TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG	300
TTCTATCTGG TTACCCCTGGA GCAAGCGCAG GAACAACAGT ACGTAGAGGG CGGTGGAGGC	360
TCCCCGGGTG AACCGTCTGG TCCAATCTCT ACTATCAACC CGTCTCCTCC GTCTAAAGAA	420

TCTCATAAAT	CTCCAAACAT	GGCTAACTGC	TCTATAATGA	TCGATGAAAT	TATACATCAC	480
TTAAAGAGAC	CACCTAACCC	TTTGCTGGAC	CCGAACAACC	TCAATTCTGA	AGACATGGAT	540
ATCCTGATGG	AACGAAACCT	TCGAACTCCA	AACCTGCTCG	CATTGTAAG	GGCTGTCAAG	600
CACTTAGAAA	ATGCATCAGG	TATTGAGGCA	ATTCTTCGTA	ATCTCCAACC	ATGTCCTGCC	660
TCTGCCACGG	CCGCACCCCTC	TCGACATCCA	ATCATCATCA	AGGCAGGTGA	CTGGCAAGAA	720
TTCCGGGAAA	AACTGACGTT	CTATCTGGTT	ACCCCTTGAGC	AAGCGCAGGA	ACAACAG	777

(2) INFORMATION FOR SEQ ID NO:65:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1047 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

ATGGCTAACT	GCTCTATAAT	GATCGATGAA	ATTATACATC	ACTTAAAGAG	ACCACCTAAC	60
CCTTGCTGG	ACCCGAACAA	CCTCAATTCT	GAAGACATGG	ATATCCTGAT	GGAACGAAAC	120
CTTCGAACTC	CAAACCTGCT	CGCATTGTA	AGGGCTGTCA	AGCACTTAGA	AAATGCATCA	180
GGTATTGAGG	CAATTCTTCG	TAATCTCAA	CCATGTCTGC	CCTCTGCCAC	GGCCGCACCC	240
TCTCGACATC	CAATCATCAT	CAAGGCAGGT	GACTGGCAAG	AATTCCGGGA	AAAACGTGACG	300
TTCTATCTGG	TTACCCCTGA	GCAAGCGCAG	GAACAACAGT	ACGTAATCGA	GGGAAGGATT	360
TCCCCCGGGC	CTCCTGTCAA	TGCTGGCGGC	GGCTCTGGTG	GTGGTTCTGG	TGGCGGCTCT	420
GAGGGTGGCG	GCTCTGAGGG	TGGCGGTTCT	GAGGGTGGCG	GCTCTGAGGG	TGGCGGTTCC	480
GGTGGCGGCT	CCGGTTCCGG	TGATTTGAT	TATGAAAACA	TGGCTACACC	ATTGGGCCCT	540
GCCAGCTCCC	TGCCCCAGAG	CTTCCTGCTC	AAGTCTTAG	AGCAAGTGAG	GAAGATCCAG	600
GGCGATGGCG	CAGCGCTCCA	GGAGAAGCTG	TGTGCCACCT	ACAAGCTGTG	CCACCCCGAG	660
GAGCTGGTGC	TGCTCGGACA	CTCTCTGGC	ATCCCCTGGG	CTCCCCCTGAG	CTCCTGCC	720
AGCCAGGCC	TGCAGCTGGC	AGGCTGCTTG	AGCCAACCTCC	ATAGCGGCCT	TTTCCTCTAC	780
CAGGGGCTCC	TGCAGGCC	GGAAAGGGATA	TCCCCCGAGT	TGGGTCCCAC	CTTGGACACA	840
CTGCAGCTGG	ACGTCGCCGA	CTTGCCACC	ACCATCTGGC	AGCAGATGGA	AGAACTGGGA	900
ATGGCCCCTG	CCCTGCAGCC	CACCCAGGGT	GCCATGCCGG	CCTTCGCC	TGCTTTCCAG	960
CGCCGGGCAG	GAGGGGCTCCT	GGTTGCTAGC	CATCTGCAGA	GCTTCCTGGA	GGTGTGTC	1020

CGCGTTCTAC GCCACCTTGC GCAGCCC

1047

(2) INFORMATION FOR SEQ ID NO:66:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 903 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTAAC	60
CCTTTGCTGG ACCCGAACAA CCTCAATTCT GAAGACATGG ATATCCTGAT GGAACGAAAC	120
CTTCGAACTC CAAACCTGCT CGCATTGTA AGGGCTGTCA AGCACTTAGA AAATGCATCA	180
GGTATTGAGG CAATTCTTCG TAATCTCAA CCATGTCTGC CCTCTGCCAC GGCGCACCC	240
TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG	300
TTCTATCTGG TTACCCCTGA GCAAGCGCAG GAACAACAGT ACGTAATCGA GGGAGGATT	360
TCCCCCGGGC CTCCTGTCAA TGCTGGCGGC GGCTCTGGTG GTGGTTCTGG TGGCGGCTCT	420
GAGGGTGGCG GCTCTGAGGG TGGCGGTTCT GAGGGTGGCG GCTCTGAGGG TGGCGGTTCC	480
GGTGGCGGCT CCGGTTCCGG TGATTTGAT TATGAAAACA TGGCACCGGC TCGTTCCCCG	540
TCCCCGTCTA CCCAGCCGTG GGAACACGTG AATGCCATCC AGGAGGCCCG GCGTCTCCTG	600
AACCTGAGTA GAGACACTGC TGCTGAGATG AATGAAACAG TAGAAGTGAT ATCAGAAATG	660
TTTGACCTCC AGGAGCCGAC TTGCCTACAG ACCCGCCTGG AGCTGTACAA GCAGGGCCTG	720
CGGGGCAGCC TCACCAAGCT CAAGGGCCCC TTGACCATGA TGGCCAGCCA CTACAAGCAG	780
CACTGCCCTC CAACCCCGGA AACTCCTGT GCAACCCAGA TTATCACCTT TGAAAGTTTC	840
AAAGAGAACCC TGAAGGACTT CCTGCTTGTC ATCCCCTTG ACTGCTGGGA GCCAGTCCAG	900
GAG	903

(2) INFORMATION FOR SEQ ID NO:67:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1017 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTAAC	60
CCTTGCTGG ACCCGAACAA CCTCAATTCT GAAGACATGG ATATCCTGAT GGAACGAAAC	120
CTTCGAACTC CAAACCTGCT CGCATTGTA AGGGCTGTCA AGCACTTAGA AAATGCATCA	180
GGTATTGAGG CAATTCTCG TAATCTCAA CCATGTCTGC CCTCTGCCAC GGCGCACCC	240
TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG	300
TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAGT ACGTAATCGA GGGAAAGGATT	360
TCCCCCGGTG CGGGCGGCTC TGGTGGTGGT TCTGGTGGCG GCTCTGAGGG TGGCGGCTCT	420
GAGGGTGGCG GTTCTGAGGG TGGCGGCTCT GAGGGTGGCG GTTCCGGTGG CGGCTCCGGT	480
TCCGGTAACA TGGCTACACC ATTAGGCCCT GCCAGCTCCC TGCCCCAGAG CTTCCTGCTC	540
AAGTGCTTAG AGCAAGTGAG GAAGATCCAG GGCGATGGCG CAGCGCTCCA GGAGAAAGCTG	600
TGTGCCACCT ACAAGCTGTG CCACCCGAG GAGCTGGTGC TGCTCGGACA CTCTCTGGC	660
ATCCCCCTGGG CTCCCTGAG CTCCCTGCCCG AGCCAGGCC TGCACTGGC AGGCTGCTTG	720
AGCCAACCTCC ATAGCGGCCT TTTCCCTTAC CAGGGGCTCC TGCAAGGCCCT GGAAGGGATA	780
TCCCCCGAGT TGGGTCCCAC CTTGGACACA CTGCAGCTGG ACGTCGCCGA CTTTGCCACC	840
ACCATCTGGC AGCAGATGGA AGAACTGGGA ATGGCCCTG CCCTGCAGCC CACCCAGGGT	900
GCCATGCCGG CCTTCGCCTC TGCTTTCCAG CGCCGGGCAG GAGGGGCTCT GGTTGCTAGC	960
CATCTGCAGA GCTTCCTGGA GGTGTCGTAC CGCGTTCTAC GCCACCTTGC GCAGCCC	1017

(2) INFORMATION FOR SEQ ID NO:68:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 966 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTAAC	60
CCTTGCTGG ACCCGAACAA CCTCAATTCT GAAGACATGG ATATCCTGAT GGAACGAAAC	120
CTTCGAACTC CAAACCTGCT CGCATTGTA AGGGCTGTCA AGCACTTAGA AAATGCATCA	180
GGTATTGAGG CAATTCTCG TAATCTCAA CCATGTCTGC CCTCTGCCAC GGCGCACCC	240
TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG	300

TTCTATCTGG TTACCCCTGGA GCAAGCGCAG GAACAACAGT ACGTAATCGA GGGAAAGGATT	360
TCCCCGGGTG AACCGTCTGG TCCAATCTCT ACTATCAACC CGTCTCCTCC GTCTAAAGAA	420
TCTCATAAAT CTCCAAACAT GGCTACACCA TTAGGCCCTG CCAGCTCCCT GCCCCAGAGC	480
TTCCTGCTCA AGTGCTTAGA GCAAGTGAGG AAGATCCAGG GCGATGGCGC AGCGCTCCAG	540
GAGAAGCTGT GTGCCACCTA CAAGCTGTGC CACCCCGAGG AGCTGGTGCT GCTCGGACAC	600
TCTCTGGGCA TCCCCTGGC TCCCCTGAGC TCCTGCCCA GCCAGGCCCT GCAGCTGGCA	660
GGCTGCTTGA GCCAACTCCA TAGCGGCCTT TTCCCTCTACC AGGGGCTCCT GCAGGCCCTG	720
GAAGGGATAT CCCCCGAGTT GGGTCCCACC TTGGACACAC TGCAGCTGGA CGTCGCCGAC	780
TTGCCACCA CCATCTGGCA GCAGATGGAA GAACTGGAA TGGCCCTGC CCTGCAGCCC	840
ACCCAGGGTG CCATGCCGGC CTTCGCCTCT GCTTCCAGC GCCGGGCAGG AGGGGTCTG	900
GTTGCTAGCC ATCTGCAGAG CTTCTGGAG GTGTCGTACC GCGTTCTACG CCACCTTGCG	960
CAGCCC	966

(2) INFORMATION FOR SEQ ID NO:69:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 822 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTAAC	60
CCTTTGCTGG ACCCGAACAA CCTCAATTCT GAAGACATGG ATATCCTGAT GGAACGAAAC	120
CTTCGAACTC CAAACCTGCT CGCATTGTA AGGGCTGTCA AGCACTTAGA AAATGCATCA	180
GGTATTGAGG CAATTCTCG TAATCTCAA CCATGTCTGC CCTCTGCCAC GGCGGCACCC	240
TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG	300
TTCTATCTGG TTACCCCTGGA GCAAGCGCAG GAACAACAGT ACGTAATCGA GGGAAAGGATT	360
TCCCCGGGTG AACCGTCTGG TCCAATCTCT ACTATCAACC CGTCTCCTCC GTCTAAAGAA	420
TCTCATAAAT CTCCAAACAT GGCACCGGCT CGTTCCCCGT CCCCCTCTAC CCAGCCGTGG	480
GAACACGTGA ATGCCATCCA GGAGGCCCCGG CGTCTCCTGA ACCTGAGTAG AGACACTGCT	540
GCTGAGATGA ATGAAACAGT AGAAGTGATA TCAGAAATGT TTGACCTCCA GGAGCCGACT	600
TGCCTACAGA CCCGCCTGGA GCTGTACAAG CAGGGCCTGC GGGGCAGCCT CACCAAGCTC	660

AAGGGCCCT	TGACCATGAT	GGCCAGCCAC	TACAAGCAGC	ACTGCCCTCC	AACCCGGAA	720
ACTTCCTGTG	CAACCCAGAT	TATCACCTT	GAAAGTTCA	AAGAGAACCT	GAAGGACTTC	780
CTGCTTGTCA	TCCCCTTGAG	CTGCTGGGAG	CCAGTCCAGG	AG		822

(2) INFORMATION FOR SEQ ID NO:70:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 966 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

ATGGCTAACT	GCTCTATAAT	GATCGATGAA	ATTATACATC	ACTTAAAGAG	ACCACCTAAC	60
CCTTGCTGG	ACCCGAACAA	CCTCAATTCT	GAAGACATGG	ATATCCTGAT	GGAACGAAAC	120
CTTCGAACTC	CAAACCTGCT	CGCATTGTA	AGGGCTGTCA	AGCACTTAGA	AAATGCATCA	180
GGTATTGAGG	CAATTCTTCG	TAATCTCCAA	CCATGTCTGC	CCTCTGCCAC	GGCCGCACCC	240
TCTCGACATC	CAATCATCAT	CAAGGCAGGT	GAATGGCAAG	AATTCCGGGA	AAAACGTGACG	300
TTCTATCTGG	TTACCCTTGA	GCAAGCGCAG	GAACAACAGT	ACGTAATCGA	GGGAAAGATT	360
TCCCCGGGTG	AACCGTCTGG	TCCAATCTCT	ACTATCAACC	CGTCTCCTCC	GTCTAAAGAA	420
TCTCATAAAAT	CTCCAAACAT	GGCTACACCA	TTAGGCCCTG	CCAGCTCCCT	GCCCCAGAGC	480
TTCCCTGCTCA	AGTGCTTAGA	GCAAGTGAGG	AAGATCCAGG	GCGATGGCGC	AGCGCTCCAG	540
GAGAAGCTGT	GTGCCACCTA	CAAGCTGTGC	CACCCCGAGG	AGCTGGTGCT	GCTCGGACAC	600
TCTCTGGGCA	TCCCCGGGC	TCCCCGTAGC	TCCTGCCCA	GCCAGGCCCT	GCAGCTGGCA	660
GGCTGCTTGA	GCCAACTCCA	TAGCGGCCCTT	TTCCTCTACC	AGGGGCTCCT	GCAGGCCCTG	720
GAAGGGATAT	CCCCCGAGTT	GGGTCCCACC	TTGGACACAC	TGCAGCTGGA	CGTCGCCGAC	780
TTTGCCACCA	CCATCTGGCA	GCAGATGGAA	GAACCTGGAA	TGGCCCTGTC	CCTGCAGCCC	840
ACCCAGGGTG	CCATGCCGGC	CTTCGCCTCT	GCTTTCCAGC	GCCGGGCAGG	AGGGGTCTCTG	900
GTTGCTAGCC	ATCTGCAGAG	CTTCCTGGAG	GTGTCGTACC	GCGTTCTACG	CCACCTTGCG	960
CAGCCC						966

(2) INFORMATION FOR SEQ ID NO:71:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 966 base pairs
 - (B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTAAC	60
CCTTTGCTGG ACCCGAACAA CCTCAATTCT GAAGACATGG ATATCCTGAT GGAACGAAAC	120
CTTCGAACTC CAAACCTGCT CGCATTGTA AGGGCTGTCA AGCACTTAGA AAATGCATCA	180
GGTATTGAGG CAATTCTCG TAATCTCAA CCATGTCTGC CCTCTGCCAC GGCGCAGACC	240
TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG	300
TTCTATCTGG TTACCCCTGGA GCAAGCGCAG GAACAAACAGT ACGTAGAGGG CGGTGGAGGC	360
TCCCCGGGTG AACCGTCTGG TCCAATCTCT ACTATCAACC CGTCTCCTCC GTCTAAAGAA	420
TCTCATAAAT CTCCAAACAT GGCTACACCA TTAGGCCCTG CCAGCTCCCT GCCCCAGAGC	480
TTCCTGCTCA AGTGCTTAGA GCAAGTGAGG AAGATCCAGG GCGATGGCGC AGCGCTCCAG	540
GAGAAGCTGT GTGCCACCTA CAAGCTGTGC CACCCGAGG AGCTGGTGCT GCTCGGACAC	600
TCTCTGGGCA TCCCCTGGC TCCCCTGAGC TCCTGCCCA GCCAGGCCCT GCAGCTGGCA	660
GGCTGCTTGA GCCAACTCCA TAGCGGCCTT TTCCTCTACC AGGGGCTCCT GCAGGCCCTG	720
GAAGGGATAT CCCCCGAGTT GGGTCCCACC TTGGACACAC TGCAGCTGGA CGTCGCCGAC	780
TTTGCCACCA CCATCTGGCA GCAGATGGAA GAACTGGAA TGGCCCTGCT CCTGCAGCCC	840
ACCCAGGGTG CCATGCCGGC CTTCGCCTCT GCTTCCAGC GCCGGGCAGG AGGGGTCCTG	900
GTTGCTAGCC ATCTGCAGAG CTTCCTGGAG GTGTCGTACC GCGTTCTACG CCACCTTGCG	960
CAGCCC	966

(2) INFORMATION FOR SEQ ID NO:72:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 921 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

ATGGCTACAC CATTAGGCCCT TGCCAGCTCC CTGCCCGAGA GCTTCCTGCT CAAGTGCTTA

60

GAGCAAGTGA	GGAAGATCCA	GGCGATGGC	GCAGCGCTCC	AGGAGAAGCT	GTGTGCCACC	120
TACAAGCTGT	GCCACCCCGA	GGAGCTGGTG	CTGCTCGGAC	ACTCTCTGGG	CATCCCTGG	180
GCTCCCTGA	GCTCCTGCC	CAGCCAGGCC	CTGCAGCTGG	CAGGCTGCTT	GAGCCAACTC	240
CATAGCGGCC	TTTCCTCTA	CCAGGGCTC	CTGCAGGCC	TGGAAGGGAT	ATCCCCGAG	300
TTGGTCCCA	CCTTGGACAC	ACTGCAGCTG	GACGTCGCCG	ACTTTGCCAC	CACCATCTGG	360
CAGCAGATGG	AAGAACTGGG	AATGGCCCT	GCCCTGCAGC	CCACCCAGGG	TGCCATGCCG	420
GCCTTCGCCT	CTGCTTCCA	GCGCCGGCA	GGAGGGTCC	TGGTTGCTAG	CCATCTGCAG	480
AGCTTCCTGG	AGGTGTCGTA	CCGCGTTCTA	CGCCACCTTG	CGCAGCCCTA	CGTAATCGAG	540
GGAAGGATT	CCCCGGGTGG	TGGTTCTGGC	GGCGGCTCCA	ACATGGCTAA	CTGCTCTATA	600
ATGATCGATG	AAATTATACA	TCACTTAAAG	AGACCACCTA	ACCCTTGCT	GGACCCGAAC	660
AACCTCAATT	CTGAAGACAT	GGATATCCTG	ATGGAACGAA	ACCTTCGAAC	TCCAAACCTG	720
CTCGCATTG	TAAGGGCTGT	CAAGCACTTA	GAAAATGCAT	CAGGTATTGA	GGCAATTCTT	780
CGTAATCTCC	AACCATGTCT	GCCCTCTGCC	ACGGCCGCAC	CCTCTCGACA	TCCAATCATC	840
ATCAAGGCAG	GTGACTGGCA	AGAATTCCGG	GAAAAACTGA	CGTTCTATCT	GGTTACCCTT	900
GAGCAAGCGC	AGGAACAACA	G				921

(2) INFORMATION FOR SEQ ID NO:73:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 966 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

ATGGCTACAC	CATTAGGCC	TGCCAGCTCC	CTGCCCCAGA	GCTTCCTGCT	CAAGTGCTTA	60
GAGCAAGTGA	GGAAGATCCA	GGCGATGGC	GCAGCGCTCC	AGGAGAAGCT	GTGTGCCACC	120
TACAAGCTGT	GCCACCCCGA	GGAGCTGGTG	CTGCTCGGAC	ACTCTCTGGG	CATCCCTGG	180
GCTCCCTGA	GCTCCTGCC	CAGCCAGGCC	CTGCAGCTGG	CAGGCTGCTT	GAGCCAACTC	240
CATAGCGGCC	TTTCCTCTA	CCAGGGCTC	CTGCAGGCC	TGGAAGGGAT	ATCCCCGAG	300
TTGGTCCCA	CCTTGGACAC	ACTGCAGCTG	GACGTCGCCG	ACTTTGCCAC	CACCATCTGG	360
CAGCAGATGG	AAGAACTGGG	AATGGCCCT	GCCCTGCAGC	CCACCCAGGG	TGCCATGCCG	420
GCCTTCGCCT	CTGCTTCCA	GCGCCGGCA	GGAGGGTCC	TGGTTGCTAG	CCATCTGCAG	480

AGCTTCCTGG AGGTGTCGTA CCGCGTTCTA CGCCACCTTG CGCAGCCCTA CGTAATCGAG	540
GGAAGGATTG CCCCGGGTGA ACCGTCTGGT CCAATCTCTA CTATCAACCC GTCTCCTCCG	600
TCTAAAGAAT CTCATAAATC TCCAAACATG GCTAACTGCT CTATAATGAT CGATGAAATT	660
ATACATCACT TAAAGAGACC ACCTAACCCCT TTGCTGGACC CGAACAAACCT CAATTCTGAA	720
GACATGGATA TCCTGATGGA ACGAAACCTT CGAACTCCAA ACCTGCTCGC ATTGTAAGG	780
GCTGTCAAGC ACTTAGAAAA TGCATCAGGT ATTGAGGCAA TTCTTCGTAAC TCTCCAACCA	840
TGTCTGCCCT CTGCCACGGC CGCACCCCTCGACATCCAA TCATCATCAA GGCAGGTGAC	900
TGGCAAGAAT TCCGGGAAAA ACTGACGTTCA TATCTGGTTA CCCTTGAGCA AGCGCAGGAA	960
CAACAG	966

(2) INFORMATION FOR SEQ ID NO:74:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1047 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

ATGGCTACAC CATTAGGCCCGGCCAGA GCTTCCTGCT CAAGTGCTTA	60
GAGCAAGTGA GGAAGATCCA GGGCGATGGC GCAGCGCTCC AGGAGAAGCT GTGTGCCACC	120
TACAAGCTGT GCCACCCCGA GGAGCTGGTCTGAGCTGGG CATCCCTGG	180
GCTCCCTGA GCTCCTGCCCGAGCCAGGCCCTGAGCTGGTCTGAGCTGGG	240
CATAGCGGCC TTTCCCTCTA CCAGGGCTCTGAGCTGGGAT ATCCCCCGAG	300
TTGGGTCCCA CCTTGGACAC ACTGCAGCTG GACGTCGCCCG ACTTTGCCAC CACCATCTGG	360
CAGCAGATGG AAGAACTGGG AATGGCCCT GCCCTGCAGC CCACCCAGGG TGCCATGCCAG	420
GCCTTCGCCT CTGCTTCCA GCGCCGGCA GGAGGGTCC TGGTTGCTAG CCATCTGCAG	480
AGCTTCCTGG AGGTGTCGTA CCGCGTTCTA CGCCACCTTG CGCAGCCCTA CGTAATCGAG	540
GGAAGGATTG CCCCCGGGCC TCCTGTCAAT GCTGGCGGCG GCTCTGGTGG TGGTTCTGGT	600
GGCGGCTCTG AGGGTGGCGG CTCTGAGGGT GGCGGTTCTG AGGGTGGCGG CTCTGAGGGT	660
GGCGGTTCCG GTGGCGGCTC CGGTTCCGGT GATTTGATT ATGAAAACAT GGCTAACTGC	720
TCTATAATGA TCGATGAAAT TATACATCAC TTAAAGAGAC CACCTAACCC TTTGCTGGAC	780
CCGAACAACC TCAATTCTGA AGACATGGAT ATCCTGATGG AACGAAACCT TCGAACTCCA	840

AACCTGCTCG CATTGTAAG GGCTGTCAAG CACTTAGAAA ATGCATCAGG TATTGAGGCA	900
ATTCTTCGTA ATCTCCAACC ATGTCTGCC CTCGCCACGG CCGCACCCCTC TCGACATCCA	960
ATCATCATCA AGGCAGGTGA CTGGCAAGAA TTCCGGAAA AACTGACGTT CTATCTGGTT	1020
ACCCTTGAGC AAGCGCAGGA ACAACAG	1047

(2) INFORMATION FOR SEQ ID NO:75:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 921 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

ATGGCTACAC CATTAGGCC CGGCCAGCTCC CTGCCAGGAGA GCTTCCTGCT CAAGTGCTTA	60
GAGCAAGTGA GGAAGATCCA GGGCGATGGC GCAGCGCTCC AGGAGAACGCT GTGTGCCACC	120
TACAAGCTGT GCCACCCCGA GGAGCTGGTG CTGCTCGGAC ACTCTCTGGG CATCCCCTGG	180
GCTCCCTGA GCTCCTGCC CAGCCAGGCC CTGCAGCTGG CAGGCTGCTT GAGCCAACTC	240
CATAGCGGCC TTTTCCTCTA CCAGGGGCTC CTGCAGGCC TGGAAGGGAT ATCCCCGAG	300
TTGGGTCCA CCTTGACAC ACTGCAGCTG GACGTCGCCG ACTTTGCCAC CACCATCTGG	360
CAGCAGATGG AAGAACTGGG AATGGCCCT GCCCTGCAGC CCACCCAGGG TGCCATGCCG	420
GCCTTCGCCT CTGCTTCCA GCGCCGGCA GGAGGGTCC TGGTTGCTAG CCATCTGCAG	480
AGCTTCCTGG AGGTGTCGTA CCGCGTTCTA CGCCACCTTG CGCAGCCCTA CGTAATCGAG	540
GGAAGGATTG CCCCAGGTGG TGGTTCTGGC GGCGGCTCCA ACATGGCTAA CTGCTCTATA	600
ATGATCGATG AAATTATACA TCACCTAAAG AGACCACCTG CACCTTGCT GGACCCGAAC	660
AACCTCAATG ACGAAGACGT CTCTATCCTG ATGGAACGAA ACCTTCGACT TCCAAACCTG	720
GAGAGCTTCG TAAGGGCTGT CAAGAACTTA GAAAATGCAT CAGGTATTGA GGCAATTCTT	780
CGTAATCTCC AACCATGTCT GCCCTCTGCC ACGGCCGCAC CCTCTCGACA TCCAATCATC	840
ATCAAGGCAG GTGACTGGCA AGAATTCCGG GAAAAACTGA CGTTCTATCT GGTTACCCTT	900
GAGCAAGCGC AGGAACAACA G	921

(2) INFORMATION FOR SEQ ID NO:76:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1047 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

ATGGCTACAC CATTAGGCCCGGCCAGA GCTTCCTGCT CAAGTGCTTA	60
GAGCAAGTGA GGAAGATCCA GGGCGATGGC GCAGCGCTCC AGGAGAAAGCT GTGTGCCACC	120
TACAAGCTGT GCCACCCCGA GGAGCTGGTG CTGCTGGAC ACTCTCTGGG CATCCCTGG	180
GCTCCCTGA GCTCCTGCCCG CAGCCAGGCC CTGCAGCTGG CAGGCTGCTT GAGCCAAC	240
CATAGCGGCC TTTTCCCTCTA CCAGGGGCTC CTGCAGGCC TGGAAGGGAT ATCCCCGAG	300
TTGGGTCCCA CCTTGGACAC ACTGCAGCTG GACGTCGCCG ACTTTGCCAC CACCATCTGG	360
CAGCAGATGG AAGAACTGGG AATGGCCCT GCCCTGCAGC CCACCCAGGG TGCCATGCCG	420
GCCTTCGCCT CTGCTTCCA GCGCCGGCA GGAGGGTCC TGGTTGCTAG CCATCTGCAG	480
AGCTTCCTGG AGGTGTCGTA CCGCGTTCTA CGCCACCTTG CGCAGCCCTA CGTAATCGAG	540
GGAAGGATTG CCCCCGGGCC TCCTGTCAAT GCTGGCGCG GCTCTGGTGG TGGTTCTGGT	600
GGCGGCTCTG AGGGTGGCGG CTCTGAGGGT GGCGGTTCTG AGGGTGGCGG CTCTGAGGGT	660
GGCGGTTCCG GTGGCGGCTC CGGTTCCGGT GATTTGATT ATGAAAACAT GGCTAACTGC	720
TCTATAATGA TCGATGAAAT TATACATCAC TTAAAGAGAC CACCTGCACC TTTGCTGGAC	780
CCGAACAACC TCAATGACGA AGACGTCTCT ATCCTGATGG AACGAAACCT TCGACTTCCA	840
AACCTGGAGA GCTTCGTAAG GGCTGTCAAG AACTTAGAAA ATGCATCAGG TATTGAGGCA	900
ATTCTTCGTA ATCTCCAACC ATGTCTGCCCG TCTGCCACGG CCGCACCCCTC TCGACATCCA	960
ATCATCATCA AGGCAGGTGA CTGGCAAGAA TTCCGGAAA AACTGACGTT CTATCTGGTT	1020
ACCCCTTGAGC AAGCGCAGGA ACAACAG	1047

(2) INFORMATION FOR SEQ ID NO:77:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 966 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

ATGGCTACAC CATTAGGCCCGGCCAGA GCTTCCTGCT CAAGTGCTTA	60
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GAGCAAGTGA	GGAAGATCCA	GGCGATGGC	GCAGCGCTCC	AGGAGAAGCT	GTGTGCCACC	120
TACAAGCTGT	GCCACCCCGA	GGAGCTGGTG	CTGCTCGGAC	ACTCTCTGGG	CATCCCTGG	180
GCTCCCTGA	GCTCCTGCC	CAGCCAGGCC	CTGCAGCTGG	CAGGCTGCTT	GAGCCAACTC	240
CATAGCGGCC	TTTCCTCTA	CCAGGGGCTC	CTGCAGGCC	TGGAAGGGAT	ATCCCCGAG	300
TTGGGTCCA	CCTTGGACAC	ACTGCAGCTG	GACGTGCGCG	ACTTTGCCAC	CACCATCTGG	360
CAGCAGATGG	AAGAACTGGG	AATGGCCCT	GCCCTGCAGC	CCACCCAGGG	TGCCATGCCG	420
GCCTTCGCCT	CTGCTTCCA	GCGCCGGCA	GGAGGGGTCC	TGGTTGCTAG	CCATCTGCAG	480
AGCTTCCTGG	AGGTGTCGTA	CCGCGTTCTA	CGCCACCTTG	CGCAGCCCTA	CGTAATCGAG	540
GGAAGGATT	CCCCGGGTGA	ACCGTCTGGT	CCAATCTCTA	CTATCAACCC	GTCTCCTCCG	600
TCTAAAGAAT	CTCATAAACATC	TCCAAACATG	GCTAACTGCT	CTATAATGAT	CGATGAAATT	660
ATACATCACT	TAAAGAGACC	ACCTGCACCT	TTGCTGGACC	CGAACAAACCT	CAATGACGAA	720
GACGTCTCTA	TCCTGATGGA	ACGAAACCTT	CGACTTCAA	ACCTGGAGAG	CTTCGTAAGG	780
GCTGTCAAGA	ACTTAGAAAA	TGCATCAGGT	ATTGAGGCAA	TTCTTCGTA	TCTCCAACCA	840
TGTCTGCCCT	CTGCCACGGC	CGCACCCCTCT	CGACATCAA	TCATCATCAA	GGCAGGTGAC	900
TGGCAAGAAT	TCCGGGAAAA	ACTGACGTT	TATCTGGTTA	CCCTTGAGCA	AGCGCAGGAA	960
CAACAG						966

(2) INFORMATION FOR SEQ ID NO:78:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 921 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

ATGGCTACAC	CATTAGGCC	TGCCAGCTCC	CTGCCCCAGA	GCTTCCTGCT	CAAGTGCTTA	60
GAGCAAGTGA	GGAAGATCCA	GGCGATGGC	GCAGCGCTCC	AGGAGAAGCT	GTGTGCCACC	120
TACAAGCTGT	GCCACCCCGA	GGAGCTGGTG	CTGCTCGGAC	ACTCTCTGGG	CATCCCTGG	180
GCTCCCTGA	GCTCCTGCC	CAGCCAGGCC	CTGCAGCTGG	CAGGCTGCTT	GAGCCAACTC	240
CATAGCGGCC	TTTCCTCTA	CCAGGGGCTC	CTGCAGGCC	TGGAAGGGAT	ATCCCCGAG	300
TTGGGTCCA	CCTTGGACAC	ACTGCAGCTG	GACGTGCGCG	ACTTTGCCAC	CACCATCTGG	360
CAGCAGATGG	AAGAACTGGG	AATGGCCCT	GCCCTGCAGC	CCACCCAGGG	TGCCATGCCG	420

GCCTTCGCCT	CTGCTTCCA	GCGCCGGCA	GGAGGGTCC	TGGTTGCTAG	CCATCTGCAG	480
AGCTTCCTGG	AGGTGTCGTA	CCGCGTTCTA	CGCCACCTTG	CGCAGCCCTA	CGTAGAGGGC	540
GGTGGAGGCT	CCCCGGGTGG	TGGTTCTGGC	GGCGGCTCCA	ACATGGCTAA	CTGCTCTATA	600
ATGATCGATG	AAATTATACA	TCACTTAAAG	AGACCACCTG	CACCTTGCT	GGACCCGAAC	660
AACCTCAATG	ACGAAGACGT	CTCTATCCTG	ATGGAACGAA	ACCTTCGACT	TCCAAACCTG	720
GAGAGCTTCG	TAAGGGCTGT	CAAGAACTTA	GAAAATGCAT	CAGGTATTGA	GGCAATTCTT	780
CGTAATCTCC	AACCATGTCT	GCCCTCTGCC	ACGGCCGCAC	CCTCTCGACA	TCCAATCATC	840
ATCAAGGCAG	GTGACTGGCA	AGAATTCCGG	GAAAAACTGA	CGTTCTATCT	GGTTACCCCTT	900
GAGCAAGCGC	AGGAACAACA	G				921

(2) INFORMATION FOR SEQ ID NO:79:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 966 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

ATGGCTACAC	CATTAGGCC	TGCCAGCTCC	CTGCCCCAGA	GCTTCCTGCT	CAAGTGCTTA	60
GAGCAAGTGA	GGAAGATCCA	GGGCGATGGC	GCAGCGCTCC	AGGAGAAAGCT	GTGTGCCACC	120
TACAAGCTGT	GCCACCCCGA	GGAGCTGGTG	CTGCTCGGAC	ACTCTCTGGG	CATCCCCCTGG	180
GCTCCCTGA	GCTCCTGCC	CAGCCAGGCC	CTGCAGCTGG	CAGGCTGCTT	GAGCCAACTC	240
CATAGCGGCC	TTTCCTCTA	CCAGGGCTC	CTGCAGGCC	TGGAAGGGAT	ATCCCCCGAG	300
TTGGGTCCCA	CCTTGGACAC	ACTGCAGCTG	GACGTGCGCG	ACTTTGCCAC	CACCATCTGG	360
CAGCAGATGG	AAGAACTGGG	AATGGCCCT	GCCCTGCAGC	CCACCCAGGG	TGCCATGCCG	420
GCCTTCGCCT	CTGCTTTCCA	GCGCCGGCA	GGAGGGGTCC	TGGTTGCTAG	CCATCTGCAG	480
AGCTTCCTGG	AGGTGTCGTA	CCGCGTTCTA	CGCCACCTTG	CGCAGCCCTA	CGTAGAGGGC	540
GGTGGAGGCT	CCCCGGGTGA	ACCGTCTGGT	CCAATCTCTA	CTATCAACCC	GTCTCCTCCG	600
TCTAAAGAAT	CTCATAAATC	TCCAAACATG	GCTAACTGCT	CTATAATGAT	CGATGAAATT	660
ATACATCACT	TAAAGAGACC	ACCTGCACCT	TTGCTGGACC	CGAACAAACCT	CAATGACGAA	720
GACGTCTCTA	TCCTGATGGA	ACGAAACCTT	CGACTTCCAA	ACCTGGAGAG	CTTCGTAAGG	780
GCTGTCAAGA	ACTTAGAAAA	TGCATCAGGT	ATTGAGGCAA	TTCTTCGTA	TCTCCAACCA	840

TGTCTGCCCT	CTGCCACGGC	CGCACCCCTCT	CGACATCCAA	TCATCATCAA	GGCAGGTGAC	900
TGGCAAGAAT	TCCGGGAAAA	ACTGACGTTTC	TATCTGGTTA	CCCTTGAGCA	AGCGCAGGAA	960
CAACAG						966

(2) INFORMATION FOR SEQ ID NO:80:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 921 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

ATGGCTACAC	CATTGGGCC	TGCCAGCTCC	CTGCCCCAGA	GCTTCCTGCT	CAAGTCTTTA	60
GAGCAAGTGA	GGAAGATCCA	GGGCGATGGC	GCAGCGCTCC	AGGAGAAAGCT	GTGTGCCACC	120
TACAAGCTGT	GCCACCCCGA	GGAGCTGGTG	CTGCTCGGAC	ACTCTCTGGG	CATCCCCTGG	180
GCTCCCTGA	GCTCCTGCC	CAGCCAGGCC	CTGCAGCTGG	CAGGCTGCTT	GAGCCAACTC	240
CATAGCGGCC	TTTCCTCTA	CCAGGGGCTC	CTGCAGGCC	TGGAAGGGAT	ATCCCCGAG	300
TTGGGTCCA	CCTTGGACAC	ACTGCAGCTG	GACGTCGCCG	ACTTGCCAC	CACCATCTGG	360
CAGCAGATGG	AAGAACTGGG	AATGGCCCT	GCCCTGCAGC	CCACCCAGGG	TGCCATGCCG	420
GCCTTCGCCT	CTGCTTCCA	GCGCCGGGCA	GGAGGGGTCC	TGGTTGCTAG	CCATCTGCAG	480
AGCTTCCTGG	AGGTGTCGTA	CCGCGTTCTA	CGCCACCTTG	CGCAGCCCTA	CGTAGAGGGC	540
GGTGGAGGCT	CCCCGGGTGG	TGGTTCTGGC	GGCGGCTCCA	ACATGGCTAA	CTGCTCTATA	600
ATGATCGATG	AAATTATACA	TCACTTAAAG	AGACCACCTG	CACCTTGCT	GGACCCGAAC	660
AACCTCAATG	ACGAAGACGT	CTCTATCCTG	ATGGAACGAA	ACCTTCGACT	TCCAAACCTG	720
GAGAGCTTCG	TAAGGGCTGT	CAAGAACTTA	GAAAATGCAT	CAGGTATTGA	GGCAATTCTT	780
CGTAATCTCC	AACCATGTCT	GCCCTCTGCC	ACGGCCGCAC	CCTCTCGACA	TCCAATCATC	840
ATCAAGGCAG	GTGACTGGCA	AGAATTCCGG	GAAAAACTGA	CGTTCTATCT	GGTTACCCCTT	900
GAGCAAGCGC	AGGAACAACA	G				921

(2) INFORMATION FOR SEQ ID NO:81:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 966 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

ATGGCTACAC CATTGGGCC CGGCCAGCTCC CTGCCAGCTCC AGGAGAAGCT GTGTGCCACC	60
TACAAGCTGT GCCACCCGA GGAGCTGGT CTGCTCGGAC ACTCTCTGGG CATCCCCTGG	120
GCTCCCTGA GCTCCTGCC CAGCCAGGCC CTGCAGCTGG CAGGCTGCTT GAGCCAAC	180
CATAGCGGCC TTTTCCCTTA CCAGGGGCTC CTGCAGGCC TGGAAGGGAT ATCCCCGAG	240
TTGGGTCCA CCTTGGACAC ACTGCAGCTG GACGTCGCCG ACTTTGCCAC CACCATCTGG	300
CAGCAGATGG AAGAACTGGG AATGGCCCCT GCCCTGCAGC CCACCCAGGG TGCCATGCCG	360
GCCTTCGCCT CTGCTTCCA GCGCCGGCA GGAGGGTCC TGGTTGCTAG CCATCTGCAG	420
AGCTTCCTGG AGGTGTCGTA CCGCGTTCTA CGCCACCTTG CGCAGCCCTA CGTAGAGGGC	480
GGTGGAGGCT CCCCGGGTGA ACCGTCTGGT CCAATCTCTA CTATCAACCC GTCTCCTCCG	540
TCTAAAGAAT CTCATAAACATC TCCAAACATG GCTAACTGCT CTATAATGAT CGATGAAATT	600
ATACATCACT TAAAGAGACC ACCTGCACCT TTGCTGGACC CGAACAAACCT CAATGACGAA	660
GACGTCTCTA TCCTGATGGA ACGAAACCTT CGACTTCAA ACCTGGAGAG CTTCGTAAGG	720
GCTGTCAAGA ACTTAGAAAA TGCATCAGGT ATTGAGGCAA TTCTTCGTAAC TCTCCAACCA	780
TGTCTGCCCT CTGCCACGGC CGCACCCCTCT CGACATCCAA TCATCATCAA GGCAAGGTGAC	840
TGGCAAGAAT TCCGGGAAAA ACTGACGTTT TATCTGGTTA CCCTTGAGCA AGCGCAGGAA	900
CAACAG	966

(2) INFORMATION FOR SEQ ID NO:82:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 777 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTGCA	60
CCTTTGCTGG ACCCGAACAA CCTCAATGAC GAAGACGTCT CTATCCTGAT GGAACGAAAC	120

CTTCGACTTC CAAACCTGGA GAGCTTCGTA AGGGCTGTCA AGAACTTAGA AAATGCATCA	180
GGTATTGAGG CAATTCTTCG TAATCTCAA CCATGTCTGC CCTCTGCCAC GGCGCACCC	240
TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG	300
TTCTATCTGG TTACCCCTGGA GCAAGCGCAG GAACAACAGT ACGTAATCGA GGGAAAGGATT	360
TCCCCGGGTG AACCGTCTGG TCCAATCTCT ACTATCAACC CGTCTCCTCC GTCTAAAGAA	420
TCTCATAAAAT CTCCAAACAT GGCTAACTGC TCTATAATGA TCGATGAAAT TATACATCAC	480
TTAAAGAGAC CACCTGCACC TTTGCTGGAC CCGAACAAACC TCAATGACGA AGACGTCTCT	540
ATCCTGATGG AACGAAACCT TCGACTTCCA AACCTGGAGA GCTTCGTAAG GGCTGTCAAG	600
AACTTAGAAA ATGCATCAGG TATTGAGGCA ATTCTTCGTA ATCTCCAACC ATGTCTGCC	660
TCTGCCACGG CCGCACCCCTC TCGACATCCA ATCATCATCA AGGCAGGTGA CTGGCAAGAA	720
TTCCGGGAAA AACTGACGTT CTATCTGGTT ACCCTTGAGC AAGCGCAGGA ACAACAG	777

(2) INFORMATION FOR SEQ ID NO:83:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 984 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTGCA	60
CCTTTGCTGG ACCCGAACAA CCTCAATGAC GAAGACGTCT CTATCCTGAT GGAACGAAAC	120
CTTCGACTTC CAAACCTGGA GAGCTTCGTA AGGGCTGTCA AGAACTTAGA AAATGCATCA	180
GGTATTGAGG CAATTCTTCG TAATCTCAA CCATGTCTGC CCTCTGCCAC GGCGCACCC	240
TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG	300
TTCTATCTGG TTACCCCTGGA GCAAGCGCAG GAACAACAGT ACGTAATCGA GGGAAAGGATT	360
TCCCCGGGTG AACCGTCTGG TCCAATCTCT ACTATCAACC CGTCTCCTCC GTCTAAAGAA	420
TCTCATAAAAT CTCCAAACAT GGCTACACCA TTGGGCCCTG CCAGCTCCCT GCCCCAGAGC	480
TTCCCTGCTCA AGTCTTTAGA GCAAGTGAGG AAGATCCAGG GCGATGGCGC AGCGCTCCAG	540
GAGAAGCTGT GTGCCACCTA CAAGCTGTGC CACCCCGAGG AGCTGGTGCT GCTCGGACAC	600
TCTCTGGGCA TCCCCTGGGC TCCCCTGAGC TCCTGCCCA GCCAGGCCCT GCAGCTGGCA	660
GGCTGCTTGA GCCAACTCCA TAGCGGCCTT TTCCTCTACC AGGGGCTCCT GCAGGCCCTG	720

GAAGGGATAT CCCCCGAGTT GGGTCCCACC TTGGACACAC TGCAGCTGGA CGTCGCCGAC	780
TTTGCCACCA CCATCTGGCA GCAGATGGAA GAACTGGAA TGGCCCTGCTC CCTGCAGCCC	840
ACCCAGGGTG CCATGCCGGC CTTGCCTCT GCTTCCAGC GCCGGGCAGG AGGGTCCTG	900
GTTGCTAGCC ATCTGCAGAG CTTCCTGGAG GTGTCGTACC GCGTTCTACG CCACCTTGCG	960
CAGCCCTGAT AAGGATCCGA ATTC	984

(2) INFORMATION FOR SEQ ID NO:84:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 921 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTGCA	60
CCTTTGCTGG ACCCGAACAA CCTCAATGAC GAAGACGTCT CTATCCTGAT GGAACGAAAC	120
CTTCGACTTC CAAACCTGGA GAGCTTCGTA AGGGCTGTCA AGAACTTAGA AAATGCATCA	180
GGTATTGAGG CAATTCTTCG TAATCTCAA CCATGTCTGC CCTCTGCCAC GGCGCACCC	240
TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG	300
TTCTATCTGG TTACCCCTGA GCAAGCGCAG GAACAACAGT ACGTAATCGA GGGAAAGGATT	360
TCCCCGGGTG GTGGTTCTGG CGGCGGCTCC AACATGGCTA CACCATTAGG CCCTGCCAGC	420
TCCCTGCCCC AGAGCTTCCT GCTCAAGTGC TTAGAGCAAG TGAGGAAGAT CCAGGGCGAT	480
GGCGCAGCGC TCCAGGAGAA GCTGTGTGCC ACCTACAAGC TGTGCCACCC CGAGGAGCTG	540
GTGCTGCTCG GACACTCTCT GGGCATCCCC TGGGCTCCCC TGAGCTCCTG CCCCAGCCAG	600
GCCCTGCAGC TGGCAGGCTG CTTGAGCCAA CTCCATAGCG GCCTTTCTCCT CTACCAGGGG	660
CTCCTGCAGG CCCTGGAAGG GATATCCCC GAGTTGGGTC CCACCTTGGAA CACACTGCAG	720
CTGGACGTGCG CCGACTTGC CACCACCATC TGGCAGCAGA TGGAAGAACT GGGAAATGGCC	780
CCTGCCCTGC AGCCCACCCA GGGTGCCATG CCGGCCTTCG CCTCTGCTTT CCAGCGCCGG	840
GCAGGAGGGG TCCTGGTTGC TAGCCATCTG CAGAGCTTCC TGGAGGTGTC GTACCGCGTT	900
CTACGCCACC TTGCGCAGCC C	921

(2) INFORMATION FOR SEQ ID NO:85:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 921 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTGCA	60
CCTTTGCTGG ACCCGAACAA CCTCAATGAC GAAGACGTCT CTATCCTGAT GGAACGAAAC	120
CTTCGACTTC CAAACCTGGA GAGCTTCGTA AGGGCTGTCA AGAACTTACA AAATGCATCA	180
GGTATTGAGG CAATTCTTCG TAATCTCAA CCATGTCTGC CCTCTGCCAC GCCGCACCC	240
TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG	300
TTCTATCTGG TTACCCCTGGA GCAAGCGCAG GAACAAACAGT ACGTAATCGA GGGAAAGGATT	360
TCCCCGGGTG GTGGTTCTGG CGGCGGCTCC AACATGGCTA CACCATTGGG CCCTGCCAGC	420
TCCCTGCCCC AGAGCTTCCT GCTCAAGTCT TTAGAGCAAG TGAGGAAGAT CCAGGGCGAT	480
GGCGCAGCGC TCCAGGAGAA GCTGTGTGCC ACCTACAAGC TGTGCCACCC CGAGGAGCTG	540
GTGCTGCTCG GACACTCTCT GGGCATCCCC TGGGCTCCCC TGAGCTCCTG CCCCAGCCAG	600
GCCCTGCAGC TGGCAGGCTG CTTGAGCAA CTCCATAGCG GCCTTTCCCT CTACCAGGGG	660
CTCCTGCAGG CCCTGGAAGG GATATCCCC GAGTTGGGTC CCACCTTGGA CACACTGCAG	720
CTGGACGTGCG CCGACTTTGC CACCACCATC TGGCAGCAGA TGGAAGAACT GGGAAATGGCC	780
CCTGCCCTGC AGCCCACCA GGGTGCCATG CGGGCCTTCG CCTCTGCTTT CCAGCGCCGG	840
GCAGGAGGGG TCCTGGTTGC TAGCCATCTG CAGAGCTTCC TGGAGGTGTC GTACCGCGTT	900
CTACGCCACC TTGCGCAGCC C	921

(2) INFORMATION FOR SEQ ID NO:86:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 732 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTGCA	60
CCTTTGCTGG ACCCGAACAA CCTCAATGAC GAAGACGTCT CTATCCTGAT GGAACGAAAC	120

CTTCGACTTC CAAACCTGGA GAGCTTCGTA AGGGCTGTCA AGAACTTAGA AAATGCATCA	180
GGTATTGAGG CAATTCTTCG TAATCTCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC	240
TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG	300
TTCTATCTGG TTACCCCTGGA GCAAGCGCAG GAACAACAGT ACGTAATCGA GGGAAAGGATT	360
TCCCCGGGTG GTGGTTCTGG CGGGGGCTCC AACATGGCTA ACTGCTCTAT AATGATCGAT	420
GAAATTATAC ATCACTTAAA GAGACCACCT GCACCTTGC TGGACCCGAA CAACCTCAAT	480
GACGAAGACG TCTCTATCCT GATGGAACGA AACCTTCGAC TTCCAAACCT GGAGAGCTTC	540
GTAAGGGCTG TCAAGAACTT AGAAAATGCA TCAGGTATTG AGGCAATTCT TCGTAATCTC	600
CAACCATGTC TGCCCTCTGC CACGGCCGCA CCCTCTCGAC ATCCAATCAT CATCAAGGCA	660
GGTGACTGGC AAGAATTCCG GGAAAAACTG ACGTTCTATC TGGTTACCCCT TGAGCAAGCG	720
CAGGAACAAAC AG	732

(2) INFORMATION FOR SEQ ID NO:87:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 921 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTGCA	60
CCTTTGCTGG ACCCGAACAA CCTCAATGAC GAAGACGTCT CTATCCTGAT GGAACGAAAC	120
CTTCGACTTC CAAACCTGGA GAGCTTCGTA AGGGCTGTCA AGAACTTAGA AAATGCATCA	180
GGTATTGAGG CAATTCTTCG TAATCTCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC	240
TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG	300
TTCTATCTGG TTACCCCTGGA GCAAGCGCAG GAACAACAGT ACGTAGAGGG CGGTGGAGGC	360
TCCCCGGGTG GTGGTTCTGG CGGGGGCTCC AACATGGCTA CACCATTGGG CCCTGCCAGC	420
TCCCTGCCCT AGAGCTTCCT GCTCAAGTCT TTAGAGCAAG TGAGGAAGAT CCAGGGCGAT	480
GGCGCAGCGC TCCAGGAGAA GCTGTGTGCC ACCTACAAGC TGTGCCACCC CGAGGAGCTG	540
GTGCTGCTCG GACACTCTCT GGGCATCCCC TGGGCTCCCC TGAGCTCTG CCCCAGCCAG	600
GCCCTGCAGC TGGCAGGCTG CTTGAGCCAA CTCCATAGCG GCCTTTCCCT CTACCAGGGG	660
CTCCTGCAGG CCCTGGAAGG GATATCCCCC GAGTTGGTC CCACCTTGGA CACACTGCAG	720

CTGGACGTCG CCGACTTTGC CACCACCATC TGGCAGCAGA TGGAAGAACT GGGAAATGGCC	780
CCTGCCCTGC AGCCCACCCA GGGTGCCATG CCGGCCTTCG CCTCTGCTTT CCAGCGCCGG	840
GCAGGAGGGG TCCTGGTTGC TAGCCATCTG CAGAGCTTCC TGGAGGTGTC GTACCGCGTT	900
CTACGCCACC TTGCGCAGCC C	921

(2) INFORMATION FOR SEQ ID NO:88:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 732 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTGCA	60
CCTTGCTGG ACCCGAACAA CCTCAATGAC GAAGACGTCT CTATCCTGAT GGAACGAAAC	120
CTTCGACTTC CAAACCTGGA GAGCTTCGTA AGGGCTGTCA AGAACTTAGA AAATGCATCA	180
GGTATTGAGG CAATTCTTCG TAATCTCAA CCATGTCTGC CCTCTGCCAC GGCGCACCC	240
TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG	300
TTCTATCTGG TTACCCCTGGA GCAAGCGCAG GAACAACAGT ACGTAGAGGG CGGTGGAGGC	360
TCCCCGGGTG GTGGTTCTGG CGGCGGCTCC AACATGGCTA ACTGCTCTAT AATGATCGAT	420
GAAATTATAC ATCACTTAAA GAGACCACCT GCACCTTTGC TGGACCCGAA CAACCTCAAT	480
GACGAAGACG TCTCTATCCT GATGGAACGA AACCTTCGAC TTCCAAACCT GGAGAGCTTC	540
GTAAGGGCTG TCAAGAACCT AGAAAATGCA TCAGGTATTG AGGCAATTCT TCGTAATCTC	600
CAACCATGTC TGCCCTCTGC CACGGCCGCA CCCTCTCGAC ATCCAATCAT CATCAAGGCA	660
GGTGACTGGC AAGAATTCCG GGAAAAACTG ACGTTCTATC TGGTTACCCCT TGAGCAAGCG	720
CAGGAACAAAC AG	732

(2) INFORMATION FOR SEQ ID NO:89:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 966 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

ATGGCTAAT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTGCA	60
CCTTGCTGG ACCCGAACAA CCTCAATGAC GAAGACGTCT CTATCCTGAT GGAACGAAAC	120
CTTCGACTTC CAAACCTGGA GAGCTTCGTA AGGGCTGTCA AGAACTTAGA AAATGCATCA	180
GGTATTGAGG CAATTCTTCG TAATCTCAA CCATGTCTGC CCTCTGCCAC GGCGCACCC	240
TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG	300
TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAGT ACGTAGAGGG CGGTGGAGGC	360
TCCCCGGGTG AACCGTCTGG TCCAATCTCT ACTATCAACC CGTCTCCTCC GTCTAAAGAA	420
TCTCATAAAT CTCCAAACAT GGCTACACCA TTGGGCCCTG CCAGCTCCCT GCCCCAGAGC	480
TTCCCTGCTCA AGTCTTTAGA GCAAGTGAGG AAGATCCAGG GCGATGGCGC AGCGCTCCAG	540
GAGAAGCTGT GTGCCACCTA CAAGCTGTGC CACCCGAGG AGCTGGTGCT GCTCGGACAC	600
TCTCTGGGCA TCCCCTGGC TCCCCTGAGC TCCTGCCCA GCCAGGCCCT GCAGCTGGCA	660
GGCTGCTTGA GCCAACTCCA TAGCGGCCTT TTCCTCTACC AGGGGCTCCT GCAGGCCCTG	720
GAAGGGATAT CCCCCGAGTT GGGTCCCACC TTGGACACAC TGCAGCTGGA CGTCGCGAC	780
TTTGCACCA CCATCTGGCA GCAGATGGAA GAACTGGAA TGGCCCTGC CCTGCAGCCC	840
ACCCAGGGTG CCATGCCGGC CTTCGCCTCT GCTTCCAGC GCCGGCAGG AGGGGTCTG	900
GTTGCTAGCC ATCTGCAGAG CTTCTGGAG GTGTCGTACC GCGTTCTACG CCACCTTGCG	960
CAGCCC	966

(2) INFORMATION FOR SEQ ID NO:90:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 777 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

ATGGCTAAT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTGCA	60
CCTTGCTGG ACCCGAACAA CCTCAATGAC GAAGACGTCT CTATCCTGAT GGAACGAAAC	120
CTTCGACTTC CAAACCTGGA GAGCTTCGTA AGGGCTGTCA AGAACTTAGA AAATGCATCA	180
GGTATTGAGG CAATTCTTCG TAATCTCAA CCATGTCTGC CCTCTGCCAC GGCGCACCC	240

TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG 300
TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAGT ACGTAGAGGG CGGTGGAGGC 360
TCCCCGGGTG AACCGTCTGG TCCAATCTCT ACTATCAACC CGTCTCCTCC GTCTAAAGAA 420
TCTCATAAAAT CTCCAAACAT GGCTAACTGC TCTATAATGA TCGATGAAAT TATACATCAC 480
TTAAAGAGAC CACCTGCACC TTTGCTGGAC CCGAACAAACC TCAATGACGA AGACGTCTCT 540
ATCCTGATGG AACGAAACCT TCGACTTCCA AACCTGGAGA GCTTCGTAAG GGCTGTCAAG 600
AACTTAGAAA ATGCATCAGG TATTGAGGCA ATTCTTCGTA ATCTCCAACC ATGTCTGCC 660
TCTGCCACGG CCGCACCCCTC TCGACATCCA ATCATCATCA AGGCAGGTGA CTGGCAAGAA 720
TTCCGGGAAA AACTGACGTT CTATCTGGTT ACCCTTGAGC AAGCGCAGGA ACAACAG 777

(2) INFORMATION FOR SEQ ID NO:91:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 41 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "synthetic DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

AATTCCGGGA AAAACTGACG TTCTATCTGG TTACCCTTGA G 41

(2) INFORMATION FOR SEQ ID NO:92:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 46 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "synthetic DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

CTGCGCTTGC TCAAGGGTAA CCAGATAGAA CGTCAGTTT TCCCGG 46

(2) INFORMATION FOR SEQ ID NO:93:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 39 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "synthetic DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

CAAGCGCAGG AACAAACAGTA CGTAATCGAG GGAAGGATT

39

(2) INFORMATION FOR SEQ ID NO:94:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 39 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "synthetic DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

ACCCGGGGAA ATCCTTCCCT CGATTACGTA CTGTTGTTC

39

(2) INFORMATION FOR SEQ ID NO:95:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 63 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "synthetic DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

TCCCCGGGTG GTGGTTCTGG CGGCGGCTCC AACATGTAAG GTACCGCATG CAAGCTTAGA

60

TCT

63

(2) INFORMATION FOR SEQ ID NO:96:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 58 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "synthetic DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

AGCTAGATCT AAGCTTGCAT GCGGTACCTT ACATGTTGGA GCCGCCGCCA GAACCACC

58

(2) INFORMATION FOR SEQ ID NO:97:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 74 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

CCGGGTGAAC CGTCTGGTCC AATCTCTACT ATCAACCCGT CTCCTCCGTC TAAAGAATCT

60

CATAAAATCTC CAAA

74

(2) INFORMATION FOR SEQ ID NO:98:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 74 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

CATGTTTGGA GATTTATGAG ATTCTTTAGA CGGAGGAGAC GGGTTGATAG TAGAGATTGG

60

ACCAAGACGGT TCAC

74

(2) INFORMATION FOR SEQ ID NO:99:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 68 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

CTAGCCATCT GCAGAGCTTC CTGGAGGTGT CGTACCGCGT TCTACGCCAC CTTGCGCAGC 60
CCTACGTA 68

(2) INFORMATION FOR SEQ ID NO:100:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 68 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "synthetic DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

AGCTTACGTA GGGCTGCGCA AGGTGGCGTA GAACGCGGTA CGACACCTCC AGGAAGCTCT 60
GCAGATGG 68

(2) INFORMATION FOR SEQ ID NO:101:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "synthetic DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

GTAATCGAGG GAAAGATTTC C 21

(2) INFORMATION FOR SEQ ID NO:102:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "synthetic DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

CCGGGGAAAT CTTTCCCTCG ATTAC 25

(2) INFORMATION FOR SEQ ID NO:103:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "synthetic DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

GTAGAGGGCG GTGGAGGCTC C

21

(2) INFORMATION FOR SEQ ID NO:104:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "synthetic DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

CCGGGGAGCC TCCACCGCCC TCTAC

25

(2) INFORMATION FOR SEQ ID NO:105:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 58 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "synthetic DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:

CATGGCACCA GCAAGATCAC CATCACCATC AACTCAACCT TGGGAACATG TGAATGCC

58

(2) INFORMATION FOR SEQ ID NO:106:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 52 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "synthetic DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

CATTCACATG TTCCCAAGGT TGAGTTGATG GTGATGGTGA TCTTGCTGGT GC

52

(2) INFORMATION FOR SEQ ID NO:107:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 66 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "synthetic DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:

CTGCCAGCTC CCTGCCCGAG AGCTTCCTGC TCAAGTCTTT AGAGCAAGTG AGGAAGATCC

60

AGGGCG

66

(2) INFORMATION FOR SEQ ID NO:108:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 66 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "synthetic DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:

CTGGATCTTC CTCACTTGCT CTAAAGACTT GAGCAGGAAG CTCTGGGCA GGGAGCTGGC

60

AGGGCC

66

(2) INFORMATION FOR SEQ ID NO:109:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 48 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "synthetic DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:

AGCTTACCTG CCATGGCTCC AGTACCACCA GGTGAAGATT CCAAAGAT

48

(2) INFORMATION FOR SEQ ID NO:110:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:

TTGGAATCTT CACCTGGTGG TACTGGAGCC ATGGCAGGTA

40

(2) INFORMATION FOR SEQ ID NO:111:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:

AGCTTCCATG GCTACCCCCC TGGGCC

26

(2) INFORMATION FOR SEQ ID NO:112:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:

CAGGGGGGTA GCCATGGA

18

(2) INFORMATION FOR SEQ ID NO:113:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "synthetic DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:113:

CATGGCTACA CCATTGGGCC

20

(2) INFORMATION FOR SEQ ID NO:114:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 12 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "synthetic DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:

CAATGGTGTA GC

12

(2) INFORMATION FOR SEQ ID NO:115:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "synthetic DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:115:

CATGGCTACA CCATTAGGAC

20

(2) INFORMATION FOR SEQ ID NO:116:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 12 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "synthetic DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:

TAATGGTGTA GC

12

(2) INFORMATION FOR SEQ ID NO:117:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "synthetic DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:117:

CCTGTCAACC CGGGCGGCGG CTCTGGTGGT

30

(2) INFORMATION FOR SEQ ID NO:118:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 31 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "synthetic DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:118:

TCATAATACA TGTTACCGGA ACGGAGCCGC C

31

(2) INFORMATION FOR SEQ ID NO:119:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 34 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "synthetic DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:119:

ATCGTCTGAC CTCCCGGGAC CTCCTGTCAA TGCT

34

(2) INFORMATION FOR SEQ ID NO:120:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:120:

AGCGTTGAC ATGTTTCAT AATCAAAATC

30

(2) INFORMATION FOR SEQ ID NO:121:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 307 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:121:

Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys
1 5 10 15

Arg Pro Pro Asn Pro Leu Leu Asp Pro Asn Asn Leu Asn Ser Glu Asp
20 25 30

Met Asp Ile Leu Met Glu Arg Asn Leu Arg Thr Pro Asn Leu Leu Ala
35 40 45

Phe Val Arg Ala Val Lys His Leu Glu Asn Ala Ser Gly Ile Glu Ala
50 55 60

Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro
65 70 75 80

Ser Arg His Pro Ile Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg
85 90 95

Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu Gln
100 105 110

Gln Tyr Val Ile Glu Gly Arg Ile Ser Pro Gly Gly Ser Gly Gly
115 120 125

Gly Ser Asn Met Ala Thr Pro Leu Gly Pro Ala Ser Ser Leu Pro Gln
 130 135 140
 Ser Phe Leu Leu Lys Cys Leu Glu Gln Val Arg Lys Ile Gln Gly Asp
 145 150 155 160
 Gly Ala Ala Leu Gln Glu Lys Leu Cys Ala Thr Tyr Lys Leu Cys His
 165 170 175
 Pro Glu Glu Leu Val Leu Leu Gly His Ser Leu Gly Ile Pro Trp Ala
 180 185 190
 Pro Leu Ser Ser Cys Pro Ser Gln Ala Leu Gln Leu Ala Gly Cys Leu
 195 200 205
 Ser Gln Leu His Ser Gly Leu Phe Leu Tyr Gln Gly Leu Leu Gln Ala
 210 215 220
 Leu Glu Gly Ile Ser Pro Glu Leu Gly Pro Thr Leu Asp Thr Leu Gln
 225 230 235 240
 Leu Asp Val Ala Asp Phe Ala Thr Thr Ile Trp Gln Gln Met Glu Glu
 245 250 255
 Leu Gly Met Ala Pro Ala Leu Gln Pro Thr Gln Gly Ala Met Pro Ala
 260 265 270
 Phe Ala Ser Ala Phe Gln Arg Arg Ala Gly Gly Val Leu Val Ala Ser
 275 280 285
 His Leu Gln Ser Phe Leu Glu Val Ser Tyr Arg Val Leu Arg His Leu
 290 295 300
 Ala Gln Pro
 305

(2) INFORMATION FOR SEQ ID NO:122:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 307 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:122:

Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys
 1 5 10 15
 Arg Pro Pro Asn Pro Leu Leu Asp Pro Asn Asn Leu Asn Ser Glu Asp
 20 25 30
 Met Asp Ile Leu Met Glu Arg Asn Leu Arg Thr Pro Asn Leu Leu Ala
 35 40 45

Phe Val Arg Ala Val Lys His Leu Glu Asn Ala Ser Gly Ile Glu Ala
 50 55 60

Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro
 65 70 75 80

Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg
 85 90 95

Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu Gln
 100 105 110

Gln Tyr Val Ile Glu Gly Arg Ile Ser Pro Gly Gly Ser Gly Gly
 115 120 125

Gly Ser Asn Met Ala Thr Pro Leu Gly Pro Ala Ser Ser Leu Pro Gln
 130 135 140

Ser Phe Leu Leu Lys Ser Leu Glu Gln Val Arg Lys Ile Gln Gly Asp
 145 150 155 160

Gly Ala Ala Leu Gln Glu Lys Leu Cys Ala Thr Tyr Lys Leu Cys His
 165 170 175

Pro Glu Glu Leu Val Leu Leu Gly His Ser Leu Gly Ile Pro Trp Ala
 180 185 190

Pro Leu Ser Ser Cys Pro Ser Gln Ala Leu Gln Leu Ala Gly Cys Leu
 195 200 205

Ser Gln Leu His Ser Gly Leu Phe Leu Tyr Gln Gly Leu Leu Gln Ala
 210 215 220

Leu Glu Gly Ile Ser Pro Glu Leu Gly Pro Thr Leu Asp Thr Leu Gln
 225 230 235 240

Leu Asp Val Ala Asp Phe Ala Thr Thr Ile Trp Gln Gln Met Glu Glu
 245 250 255

Leu Gly Met Ala Pro Ala Leu Gln Pro Thr Gln Gly Ala Met Pro Ala
 260 265 270

Phe Ala Ser Ala Phe Gln Arg Arg Ala Gly Gly Val Leu Val Ala Ser
 275 280 285

His Leu Gln Ser Phe Leu Glu Val Ser Tyr Arg Val Leu Arg His Leu
 290 295 300

Ala Gln Pro
 305

(2) INFORMATION FOR SEQ ID NO:123:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 307 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:123:

Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His His Leu Lys
1 5 10 15

Arg Pro Pro Asn Pro Leu Leu Asp Pro Asn Asn Leu Asn Ser Glu Asp
20 25 30

Met Asp Ile Leu Met Glu Arg Asn Leu Arg Thr Pro Asn Leu Leu Ala
35 40 45

Phe Val Arg Ala Val Lys His Leu Glu Asn Ala Ser Gly Ile Glu Ala
50 55 60

Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro
65 70 75 80

Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg
85 90 95

Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu Gln
100 105 110

Gln Tyr Val Ile Glu Gly Lys Ile Ser Pro Gly Gly Ser Gly Gly
115 120 125

Gly Ser Asn Met Ala Thr Pro Leu Gly Pro Ala Ser Ser Leu Pro Gln
130 135 140

Ser Phe Leu Leu Lys Ser Leu Glu Gln Val Arg Lys Ile Gln Gly Asp
145 150 155 160

Gly Ala Ala Leu Gln Glu Lys Leu Cys Ala Thr Tyr Lys Leu Cys His
165 170 175

Pro Glu Glu Leu Val Leu Leu Gly His Ser Leu Gly Ile Pro Trp Ala
180 185 190

Pro Leu Ser Ser Cys Pro Ser Gln Ala Leu Gln Leu Ala Gly Cys Leu
195 200 205

Ser Gln Leu His Ser Gly Leu Phe Leu Tyr Gln Gly Leu Leu Gln Ala
210 215 220

Leu Glu Gly Ile Ser Pro Glu Leu Gly Pro Thr Leu Asp Thr Leu Gln
225 230 235 240

Leu Asp Val Ala Asp Phe Ala Thr Thr Ile Trp Gln Gln Met Glu Glu
245 250 255

Leu Gly Met Ala Pro Ala Leu Gln Pro Thr Gln Gly Ala Met Pro Ala
260 265 270

Phe Ala Ser Ala Phe Gln Arg Arg Ala Gly Gly Val Leu Val Ala Ser
275 280 285

His Leu Gln Ser Phe Leu Glu Val Ser Tyr Arg Val Leu Arg His Leu
290 295 300

Ala Gln Pro
305

(2) INFORMATION FOR SEQ ID NO:124:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 307 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:124:

Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His His Leu Lys
1 5 10 15

Arg Pro Pro Asn Pro Leu Leu Asp Pro Asn Asn Leu Asn Ser Glu Asp
20 25 30

Met Asp Ile Leu Met Glu Arg Asn Leu Arg Thr Pro Asn Leu Leu Ala
35 40 45

Phe Val Arg Ala Val Lys His Leu Glu Asn Ala Ser Gly Ile Glu Ala
50 55 60

Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro
65 70 75 80

Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg
85 90 95

Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu Gln
100 105 110

Gln Tyr Val Glu Gly Gly Ser Pro Gly Gly Ser Gly Gly
115 120 125

Gly Ser Asn Met Ala Thr Pro Leu Gly Pro Ala Ser Ser Leu Pro Gln
130 135 140

Ser Phe Leu Leu Lys Ser Leu Glu Gln Val Arg Lys Ile Gln Gly Asp
145 150 155 160

Gly Ala Ala Leu Gln Glu Lys Leu Cys Ala Thr Tyr Lys Leu Cys His
165 170 175

Pro Glu Glu Leu Val Leu Leu Gly His Ser Leu Gly Ile Pro Trp Ala
180 185 190

Pro Leu Ser Ser Cys Pro Ser Gln Ala Leu Gln Leu Ala Gly Cys Leu
195 200 205

Ser Gln Leu His Ser Gly Leu Phe Leu Tyr Gln Gly Leu Leu Gln Ala
210 215 220

Leu Glu Gly Ile Ser Pro Glu Leu Gly Pro Thr Leu Asp Thr Leu Gln
225 230 235 240

Leu Asp Val Ala Asp Phe Ala Thr Thr Ile Trp Gln Gln Met Glu Glu
245 250 255

Leu Gly Met Ala Pro Ala Leu Gln Pro Thr Gln Gly Ala Met Pro Ala
260 265 270

Phe Ala Ser Ala Phe Gln Arg Arg Ala Gly Gly Val Leu Val Ala Ser
275 280 285

His Leu Gln Ser Phe Leu Glu Val Ser Tyr Arg Val Leu Arg His Leu
290 295 300

Ala Gln Pro
305

(2) INFORMATION FOR SEQ ID NO:125:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 244 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:125:

Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys
1 5 10 15

Arg Pro Pro Asn Pro Leu Leu Asp Pro Asn Asn Leu Asn Ser Glu Asp
20 25 30

Met Asp Ile Leu Met Glu Arg Asn Leu Arg Thr Pro Asn Leu Leu Ala
35 40 45

Phe Val Arg Ala Val Lys His Leu Glu Asn Ala Ser Gly Ile Glu Ala
50 55 60

Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro
65 70 75 80

Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg
85 90 95

Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu Gln
100 105 110

Gln Tyr Val Ile Glu Gly Arg Ile Ser Pro Gly Gly Ser Gly Gly
115 120 125

Gly Ser Asn Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His
130 135 140

His Leu Lys Arg Pro Pro Asn Pro Leu Leu Asp Pro Asn Asn Leu Asn

145	150	155	160
Ser Glu Asp Met Asp Ile Leu Met Glu Arg Asn Leu Arg Thr Pro Asn			
165 170 175			
Leu Leu Ala Phe Val Arg Ala Val Lys His Leu Glu Asn Ala Ser Gly			
180 185 190			
Ile Glu Ala Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr			
195 200 205			
Ala Ala Pro Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln			
210 215 220			
Glu Phe Arg Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala			
225 230 235 240			
Gln Glu Gln Gln			

(2) INFORMATION FOR SEQ ID NO:126:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 244 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:126:

Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys	15		
1	5	10	
Arg Pro Pro Asn Pro Leu Leu Asp Pro Asn Asn Leu Asn Ser Glu Asp	30		
20	25	30	
Met Asp Ile Leu Met Glu Arg Asn Leu Arg Thr Pro Asn Leu Leu Ala	45		
35	40	45	
Phe Val Arg Ala Val Lys His Leu Glu Asn Ala Ser Gly Ile Glu Ala	60		
50	55	60	
Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro	80		
65	70	75	80
Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg	95		
85	90	95	
Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu Gln	110		
100	105	110	
Gln Tyr Val Ile Glu Gly Lys Ile Ser Pro Gly Gly Ser Gly Gly	125		
115	120	125	
Gly Ser Asn Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His	140		
130	135	140	

His Leu Lys Arg Pro Pro Asn Pro Leu Leu Asp Pro Asn Asn Leu Asn
 145 150 155 160
 Ser Glu Asp Met Asp Ile Leu Met Glu Arg Asn Leu Arg Thr Pro Asn
 165 170 175
 Leu Leu Ala Phe Val Arg Ala Val Lys His Leu Glu Asn Ala Ser Gly
 180 185 190
 Ile Glu Ala Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr
 195 200 205
 Ala Ala Pro Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln
 210 215 220
 Glu Phe Arg Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala
 225 230 235 240
 Gln Glu Gln Gln

(2) INFORMATION FOR SEQ ID NO:127:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 244 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:127:

Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His His Leu Lys
 1 5 10 15
 Arg Pro Pro Asn Pro Leu Leu Asp Pro Asn Asn Leu Asn Ser Glu Asp
 20 25 30
 Met Asp Ile Leu Met Glu Arg Asn Leu Arg Thr Pro Asn Leu Leu Ala
 35 40 45
 Phe Val Arg Ala Val Lys His Leu Glu Asn Ala Ser Gly Ile Glu Ala
 50 55 60
 Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro
 65 70 75 80
 Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg
 85 90 95
 Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu Gln
 100 105 110
 Gln Tyr Val Glu Gly Gly Gly Ser Pro Gly Gly Ser Gly Gly
 115 120 125

Gly Ser Asn Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His
130 135 140

His Leu Lys Arg Pro Pro Asn Pro Leu Leu Asp Pro Asn Asn Leu Asn
145 150 155 160

Ser Glu Asp Met Asp Ile Leu Met Glu Arg Asn Leu Arg Thr Pro Asn
165 170 175

Leu Leu Ala Phe Val Arg Ala Val Lys His Leu Glu Asn Ala Ser Gly
180 185 190

Ile Glu Ala Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr
195 200 205

Ala Ala Pro Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln
210 215 220

Glu Phe Arg Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala
225 230 235 240

Gln Glu Gln Gln

(2) INFORMATION FOR SEQ ID NO:128:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 322 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:128:

Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys
1 5 10 15

Arg Pro Pro Asn Pro Leu Leu Asp Pro Asn Asn Leu Asn Ser Glu Asp
20 25 30

Met Asp Ile Leu Met Glu Arg Asn Leu Arg Thr Pro Asn Leu Leu Ala
35 40 45

Phe Val Arg Ala Val Lys His Leu Glu Asn Ala Ser Gly Ile Glu Ala
50 55 60

Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro
65 70 75 80

Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg
85 90 95

Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu Gln
100 105 110

Gln Tyr Val Ile Glu Gly Arg Ile Ser Pro Gly Glu Pro Ser Gly Pro

115

120

125

Ile Ser Thr Ile Asn Pro Ser Pro Pro Ser Lys Glu Ser His His Lys Ser
 130 135 140

Pro Asn Met Ala Thr Pro Leu Gly Pro Ala Ser Ser Leu Pro Gln Ser
 145 150 155 160

Phe Leu Leu Lys Cys Leu Glu Gln Val Arg Lys Ile Gln Gly Asp Gly
 165 170 175

Ala Ala Leu Gln Glu Lys Leu Cys Ala Thr Tyr Lys Leu Cys His Pro
 180 185 190

Glu Glu Leu Val Leu Leu Gly His Ser Leu Gly Ile Pro Trp Ala Pro
 195 200 205

Leu Ser Ser Cys Pro Ser Gln Ala Leu Gln Leu Ala Gly Cys Leu Ser
 210 215 220

Gln Leu His Ser Gly Leu Phe Leu Tyr Gln Gly Leu Leu Gln Ala Leu
 225 230 235 240

Glu Gly Ile Ser Pro Glu Leu Gly Pro Thr Leu Asp Thr Leu Gln Leu
 245 250 255

Asp Val Ala Asp Phe Ala Thr Thr Ile Trp Gln Gln Met Glu Glu Leu
 260 265 270

Gly Met Ala Pro Ala Leu Gln Pro Thr Gln Gly Ala Met Pro Ala Phe
 275 280 285

Ala Ser Ala Phe Gln Arg Arg Ala Gly Gly Val Leu Val Ala Ser His
 290 295 300

Leu Gln Ser Phe Leu Glu Val Ser Tyr Arg Val Leu Arg His Leu Ala
 305 310 315 320

Gln Pro

(2) INFORMATION FOR SEQ ID NO:129:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 322 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:129:

Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys
 1 5 10 15

Arg Pro Pro Asn Pro Leu Leu Asp Pro Asn Asn Leu Asn Ser Glu Asp
 20 25 30

Met Asp Ile Leu Met Glu Arg Asn Leu Arg Thr Pro Asn Leu Leu Ala
 35 40 45

Phe Val Arg Ala Val Lys His Leu Glu Asn Ala Ser Gly Ile Glu Ala
 50 55 60

Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro
 65 70 75 80

Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg
 85 90 95

Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu Gln
 100 105 110

Gln Tyr Val Ile Glu Gly Lys Ile Ser Pro Gly Glu Pro Ser Gly Pro
 115 120 125

Ile Ser Thr Ile Asn Pro Ser Pro Pro Ser Lys Glu Ser His Lys Ser
 130 135 140

Pro Asn Met Ala Thr Pro Leu Gly Pro Ala Ser Ser Leu Pro Gln Ser
 145 150 155 160

Phe Leu Leu Lys Cys Leu Glu Gln Val Arg Lys Ile Gln Gly Asp Gly
 165 170 175

Ala Ala Leu Gln Glu Lys Leu Cys Ala Thr Tyr Lys Leu Cys His Pro
 180 185 190

Glu Glu Leu Val Leu Leu Gly His Ser Leu Gly Ile Pro Trp Ala Pro
 195 200 205

Leu Ser Ser Cys Pro Ser Gln Ala Leu Gln Leu Ala Gly Cys Leu Ser
 210 215 220

Gln Leu His Ser Gly Leu Phe Leu Tyr Gln Gly Leu Leu Gln Ala Leu
 225 230 235 240

Glu Gly Ile Ser Pro Glu Leu Gly Pro Thr Leu Asp Thr Leu Gln Leu
 245 250 255

Asp Val Ala Asp Phe Ala Thr Thr Ile Trp Gln Gln Met Glu Glu Leu
 260 265 270

Gly Met Ala Pro Ala Leu Gln Pro Thr Gln Gly Ala Met Pro Ala Phe
 275 280 285

Ala Ser Ala Phe Gln Arg Arg Ala Gly Gly Val Leu Val Ala Ser His
 290 295 300

Leu Gln Ser Phe Leu Glu Val Ser Tyr Arg Val Leu Arg His Leu Ala
 305 310 315 320

Gln Pro

(2) INFORMATION FOR SEQ ID NO:130:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 322 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:130:

Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys
1 5 10 15

Arg Pro Pro Asn Pro Leu Leu Asp Pro Asn Asn Leu Asn Ser Glu Asp
20 25 30

Met Asp Ile Leu Met Glu Arg Asn Leu Arg Thr Pro Asn Leu Leu Ala
35 40 45

Phe Val Arg Ala Val Lys His Leu Glu Asn Ala Ser Gly Ile Glu Ala
50 55 60

Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro
65 70 75 80

Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg
85 90 95

Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu Gln
100 105 110

Gln Tyr Val Glu Gly Gly Ser Pro Gly Glu Pro Ser Gly Pro
115 120 125

Ile Ser Thr Ile Asn Pro Ser Pro Ser Lys Glu Ser His Lys Ser
130 135 140

Pro Asn Met Ala Thr Pro Leu Gly Pro Ala Ser Ser Leu Pro Gln Ser
145 150 155 160

Phe Leu Leu Lys Cys Leu Glu Gln Val Arg Lys Ile Gln Gly Asp Gly
165 170 175

Ala Ala Leu Gln Glu Lys Leu Cys Ala Thr Tyr Lys Leu Cys His Pro
180 185 190

Glu Glu Leu Val Leu Leu Gly His Ser Leu Gly Ile Pro Trp Ala Pro
195 200 205

Leu Ser Ser Cys Pro Ser Gln Ala Leu Gln Leu Ala Gly Cys Leu Ser
210 215 220

Gln Leu His Ser Gly Leu Phe Leu Tyr Gln Gly Leu Leu Gln Ala Leu
225 230 235 240

Glu Gly Ile Ser Pro Glu Leu Gly Pro Thr Leu Asp Thr Leu Gln Leu
245 250 255

Asp Val Ala Asp Phe Ala Thr Thr Ile Trp Gln Gln Met Glu Glu Leu

260

265

270

Gly Met Ala Pro Ala Leu Gln Pro Thr Gln Gly Ala Met Pro Ala Phe
275 280 285

Ala Ser Ala Phe Gln Arg Arg Ala Gly Gly Val Leu Val Ala Ser His
290 295 300

Leu Gln Ser Phe Leu Glu Val Ser Tyr Arg Val Leu Arg His Leu Ala
305 310 315 320

Gln Pro

(2) INFORMATION FOR SEQ ID NO:131:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 259 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:131:

Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys
1 5 10 15

Arg Pro Pro Asn Pro Leu Leu Asp Pro Asn Asn Leu Asn Ser Glu Asp
20 25 30

Met Asp Ile Leu Met Glu Arg Asn Leu Arg Thr Pro Asn Leu Leu Ala
35 40 45

Phe Val Arg Ala Val Lys His Leu Glu Asn Ala Ser Gly Ile Glu Ala
50 55 60

Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro
65 70 75 80

Ser Arg His Pro Ile Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg
85 90 95

Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu Gln
100 105 110

Gln Tyr Val Ile Glu Gly Arg Ile Ser Pro Gly Glu Pro Ser Gly Pro
115 120 125

Ile Ser Thr Ile Asn Pro Ser Pro Pro Ser Lys Glu Ser His Lys Ser
130 135 140

Pro Asn Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His
145 150 155 160

Leu Lys Arg Pro Pro Asn Pro Leu Leu Asp Pro Asn Asn Leu Asn Ser
165 170 175

Glu Asp Met Asp Ile Leu Met Glu Arg Asn Leu Arg Thr Pro Asn Leu
180 185 190
Leu Ala Phe Val Arg Ala Val Lys His Leu Glu Asn Ala Ser Gly Ile
195 200 205
Glu Ala Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala
210 215 220
Ala Pro Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu
225 230 235 240
Phe Arg Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln
245 250 255
Glu Gln Gln

(2) INFORMATION FOR SEQ ID NO:132:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 259 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:132:

Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys
1 5 10 15
Arg Pro Pro Asn Pro Leu Leu Asp Pro Asn Asn Leu Asn Ser Glu Asp
20 25 30
Met Asp Ile Leu Met Glu Arg Asn Leu Arg Thr Pro Asn Leu Leu Ala
35 40 45
Phe Val Arg Ala Val Lys His Leu Glu Asn Ala Ser Gly Ile Glu Ala
50 55 60
Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro
65 70 75 80
Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg
85 90 95
Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu Gln
100 105 110
Gln Tyr Val Ile Glu Gly Lys Ile Ser Pro Gly Glu Pro Ser Gly Pro
115 120 125
Ile Ser Thr Ile Asn Pro Ser Pro Pro Ser Lys Glu Ser His Lys Ser
130 135 140

Pro Asn Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His
 145 150 155 160
 Leu Lys Arg Pro Pro Asn Pro Leu Leu Asp Pro Asn Asn Leu Asn Ser
 165 170 175
 Glu Asp Met Asp Ile Leu Met Glu Arg Asn Leu Arg Thr Pro Asn Leu
 180 185 190
 Leu Ala Phe Val Arg Ala Val Lys His Leu Glu Asn Ala Ser Gly Ile
 195 200 205
 Glu Ala Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala
 210 215 220
 Ala Pro Ser Arg His Pro Ile Ile Lys Ala Gly Asp Trp Gln Glu
 225 230 235 240
 Phe Arg Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln
 245 250 255
 Glu Gln Gln

(2) INFORMATION FOR SEQ ID NO:133:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 259 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:133:

Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys
 1 5 10 15
 Arg Pro Pro Asn Pro Leu Leu Asp Pro Asn Asn Leu Asn Ser Glu Asp
 20 25 30
 Met Asp Ile Leu Met Glu Arg Asn Leu Arg Thr Pro Asn Leu Leu Ala
 35 40 45
 Phe Val Arg Ala Val Lys His Leu Glu Asn Ala Ser Gly Ile Glu Ala
 50 55 60
 Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro
 65 70 75 80
 Ser Arg His Pro Ile Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg
 85 90 95
 Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu Gln
 100 105 110
 Gln Tyr Val Glu Gly Gly Ser Pro Gly Glu Pro Ser Gly Pro

115

120

125

Ile Ser Thr Ile Asn Pro Ser Pro Pro Ser Lys Glu Ser His Lys Ser
 130 135 140

Pro Asn Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His
 145 150 155 160

Leu Lys Arg Pro Pro Asn Pro Leu Leu Asp Pro Asn Asn Leu Asn Ser
 165 170 175

Glu Asp Met Asp Ile Leu Met Glu Arg Asn Leu Arg Thr Pro Asn Leu
 180 185 190

Leu Ala Phe Val Arg Ala Val Lys His Leu Glu Asn Ala Ser Gly Ile
 195 200 205

Glu Ala Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala
 210 215 220

Ala Pro Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu
 225 230 235 240

Phe Arg Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln
 245 250 255

Glu Gln Gln

(2) INFORMATION FOR SEQ ID NO:134:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 307 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:134:

Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys
 1 5 10 15

Arg Pro Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn Asp Glu Asp
 20 25 30

Val Ser Ile Leu Met Asp Arg Asn Leu Arg Leu Pro Asn Leu Glu Ser
 35 40 45

Phe Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Gly Ile Glu Ala
 50 55 60

Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro
 65 70 75 80

Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg
 85 90 95

Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu Gln
 100 105 110
 Gln Tyr Val Ile Glu Gly Arg Ile Ser Pro Gly Gly Ser Gly Gly
 115 120 125
 Gly Ser Asn Met Ala Thr Pro Leu Gly Pro Ala Ser Ser Leu Pro Gln
 130 135 140
 Ser Phe Leu Leu Lys Cys Leu Glu Gln Val Arg Lys Ile Gln Gly Asp
 145 150 155 160
 Gly Ala Ala Leu Gln Glu Lys Leu Cys Ala Thr Tyr Lys Leu Cys His
 165 170 175
 Pro Glu Glu Leu Val Leu Leu Gly His Ser Leu Gly Ile Pro Trp Ala
 180 185 190
 Pro Leu Ser Ser Cys Pro Ser Gln Ala Leu Gln Leu Ala Gly Cys Leu
 195 200 205
 Ser Gln Leu His Ser Gly Leu Phe Leu Tyr Gln Gly Leu Leu Gln Ala
 210 215 220
 Leu Glu Gly Ile Ser Pro Glu Leu Gly Pro Thr Leu Asp Thr Leu Gln
 225 230 235 240
 Leu Asp Val Ala Asp Phe Ala Thr Thr Ile Trp Gln Gln Met Glu Glu
 245 250 255
 Leu Gly Met Ala Pro Ala Leu Gln Pro Thr Gln Gly Ala Met Pro Ala
 260 265 270
 Phe Ala Ser Ala Phe Gln Arg Arg Ala Gly Gly Val Leu Val Ala Ser
 275 280 285
 His Leu Gln Ser Phe Leu Glu Val Ser Tyr Arg Val Leu Arg His Leu
 290 295 300
 Ala Gln Pro
 305

(2) INFORMATION FOR SEQ ID NO:135:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 307 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:135:

Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys
 1 5 10 15

Arg Pro Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn Asp Glu Asp
 20 25 30
 Val Ser Ile Leu Met Asp Arg Asn Leu Arg Leu Pro Asn Leu Glu Ser
 35 40 45
 Phe Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Gly Ile Glu Ala
 50 55 60
 Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro
 65 70 75 80
 Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg
 85 90 95
 Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu Gln
 100 105 110
 Gln Tyr Val Ile Glu Gly Arg Ile Ser Pro Gly Gly Ser Gly Gly
 115 120 125
 Gly Ser Asn Met Ala Thr Pro Leu Gly Pro Ala Ser Ser Leu Pro Gln
 130 135 140
 Ser Phe Leu Leu Lys Ser Leu Glu Gln Val Arg Lys Ile Gln Gly Asp
 145 150 155 160
 Gly Ala Ala Leu Gln Glu Lys Leu Cys Ala Thr Tyr Lys Leu Cys His
 165 170 175
 Pro Glu Glu Leu Val Leu Leu Gly His Ser Leu Gly Ile Pro Trp Ala
 180 185 190
 Pro Leu Ser Ser Cys Pro Ser Gln Ala Leu Gln Leu Ala Gly Cys Leu
 195 200 205
 Ser Gln Leu His Ser Gly Leu Phe Leu Tyr Gln Gly Leu Leu Gln Ala
 210 215 220
 Leu Glu Gly Ile Ser Pro Glu Leu Gly Pro Thr Leu Asp Thr Leu Gln
 225 230 235 240
 Leu Asp Val Ala Asp Phe Ala Thr Thr Ile Trp Gln Gln Met Glu Glu
 245 250 255
 Leu Gly Met Ala Pro Ala Leu Gln Pro Thr Gln Gly Ala Met Pro Ala
 260 265 270
 Phe Ala Ser Ala Phe Gln Arg Arg Ala Gly Gly Val Leu Val Ala Ser
 275 280 285
 His Leu Gln Ser Phe Leu Glu Val Ser Tyr Arg Val Leu Arg His Leu
 290 295 300
 Ala Gln Pro
 305

(2) INFORMATION FOR SEQ ID NO:136:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 244 amino acids

(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:136:

Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys
1 5 10 15

Arg Pro Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn Asp Glu Asp
20 25 30

Val Ser Ile Leu Met Asp Arg Asn Leu Arg Leu Pro Asn Leu Glu Ser
35 40 45

Phe Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Gly Ile Glu Ala
50 55 60

Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro
65 70 75 80

Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg
85 90 95

Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu Gln
100 105 110

Gln Tyr Val Ile Glu Gly Arg Ile Ser Pro Gly Gly Ser Gly Gly
115 120 125

Gly Ser Asn Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His
130 135 140

His Leu Lys Arg Pro Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn
145 150 155 160

Asp Glu Asp Val Ser Ile Leu Met Asp Arg Asn Leu Arg Leu Pro Asn
165 170 175

Leu Glu Ser Phe Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Gly
180 185 190

Ile Glu Ala Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr
195 200 205

Ala Ala Pro Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln
210 215 220

Glu Phe Arg Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala
225 230 235 240

Gln Glu Gln Gln

(2) INFORMATION FOR SEQ ID NO:137:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 259 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:137:

Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys
1 5 10 15

Arg Pro Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn Asp Glu Asp
20 25 30

Val Ser Ile Leu Met Asp Arg Asn Leu Arg Leu Pro Asn Leu Glu Ser
35 40 45

Phe Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Gly Ile Glu Ala
50 55 60

Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro
65 70 75 80

Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg
85 90 95

Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu Gln
100 105 110

Gln Tyr Val Ile Glu Gly Arg Ile Ser Pro Gly Glu Pro Ser Gly Pro
115 120 125

Ile Ser Thr Ile Asn Pro Ser Pro Pro Ser Lys Glu Ser His Lys Ser
130 135 140

Pro Asn Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His
145 150 155 160

Leu Lys Arg Pro Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn Asp
165 170 175

Glu Asp Val Ser Ile Leu Met Asp Arg Asn Leu Arg Leu Pro Asn Leu
180 185 190

Glu Ser Phe Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Gly Ile
195 200 205

Glu Ala Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala
210 215 220

Ala Pro Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu
225 230 235 240

Phe Arg Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln
245 250 255

Glu Gln Gln

(2) INFORMATION FOR SEQ ID NO:138:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 322 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:138:

Met	Ala	Asn	Cys	Ser	Ile	Met	Ile	Asp	Glu	Ile	Ile	His	His	Leu	Lys
1						5				10				15	
Arg	Pro	Pro	Ala	Pro	Leu	Leu	Asp	Pro	Asn	Asn	Leu	Asn	Asp	Glu	Asp
					20			25					30		
Val	Ser	Ile	Leu	Met	Asp	Arg	Asn	Leu	Arg	Leu	Pro	Asn	Leu	Glu	Ser
							35		40				45		
Phe	Val	Arg	Ala	Val	Lys	Asn	Leu	Glu	Asn	Ala	Ser	Gly	Ile	Glu	Ala
						50		55				60			
Ile	Leu	Arg	Asn	Leu	Gln	Pro	Cys	Leu	Pro	Ser	Ala	Thr	Ala	Ala	Pro
						65		70		75			80		
Ser	Arg	His	Pro	Ile	Ile	Ile	Lys	Ala	Gly	Asp	Trp	Gln	Glu	Phe	Arg
						85			90				95		
Glu	Lys	Leu	Thr	Phe	Tyr	Leu	Val	Thr	Leu	Glu	Gln	Ala	Gln	Glu	Gln
						100			105				110		
Gln	Tyr	Val	Ile	Glu	Gly	Arg	Ile	Ser	Pro	Gly	Glu	Pro	Ser	Gly	Pro
							115		120				125		
Ile	Ser	Thr	Ile	Asn	Pro	Ser	Pro	Pro	Ser	Lys	Glu	Ser	His	Lys	Ser
						130		135				140			
Pro	Asn	Met	Ala	Thr	Pro	Leu	Gly	Pro	Ala	Ser	Ser	Leu	Pro	Gln	Ser
							145		150			155		160	
Phe	Leu	Leu	Lys	Ser	Leu	Glu	Gln	Val	Arg	Lys	Ile	Gln	Gly	Asp	Gly
							165			170			175		
Ala	Ala	Leu	Gln	Glu	Lys	Leu	Cys	Ala	Thr	Tyr	Lys	Leu	Cys	His	Pro
							180			185			190		
Glu	Glu	Leu	Val	Leu	Leu	Gly	His	Ser	Leu	Gly	Ile	Pro	Trp	Ala	Pro
							195		200				205		
Leu	Ser	Ser	Cys	Pro	Ser	Gln	Ala	Leu	Gln	Leu	Ala	Gly	Cys	Leu	Ser
							210			215			220		
Gln	Leu	His	Ser	Gly	Leu	Phe	Leu	Tyr	Gln	Gly	Leu	Leu	Gln	Ala	Leu

225	230	235	240
Glu Gly Ile Ser Pro Glu Leu Gly Pro Thr Leu Asp Thr Leu Gln Leu			
245		250	255
Asp Val Ala Asp Phe Ala Thr Thr Ile Trp Gln Gln Met Glu Glu Leu			
260		265	270
Gly Met Ala Pro Ala Leu Gln Pro Thr Gln Gly Ala Met Pro Ala Phe			
275		280	285
Ala Ser Ala Phe Gln Arg Arg Ala Gly Gly Val Leu Val Ala Ser His			
290		295	300
Leu Gln Ser Phe Leu Glu Val Ser Tyr Arg Val Leu Arg His Leu Ala			
305		310	315
Gln Pro			

(2) INFORMATION FOR SEQ ID NO:139:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 349 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:139:

Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His His Leu Lys			
1	5	10	15
Arg Pro Pro Asn Pro Leu Leu Asp Pro Asn Asn Leu Asn Ser Glu Asp			
20		25	30
Met Asp Ile Leu Met Glu Arg Asn Leu Arg Thr Pro Asn Leu Leu Ala			
35		40	45
Phe Val Arg Ala Val Lys His Leu Glu Asn Ala Ser Gly Ile Glu Ala			
50		55	60
Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro			
65		70	75
Ser Arg His Pro Ile Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg			
85		90	95
Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu Gln			
100		105	110
Gln Tyr Val Ile Glu Gly Arg Ile Ser Pro Gln Pro Pro Val Asn Ala			
115		120	125
Gly Gly Gly Ser Gly Gly Ser Gly Gly Ser Glu Gly Gly Gly			
130		135	140

Ser Glu Gly Gly Ser Glu Gly Gly Ser Glu Gly Gly Ser
 145 150 155 160
 Gly Gly Gly Ser Gly Ser Gly Asp Phe Asp Tyr Glu Asn Met Ala Thr
 165 170 175
 Pro Leu Gly Pro Ala Ser Ser Leu Pro Gln Ser Phe Leu Leu Lys Ser
 180 185 190
 Leu Glu Gln Val Arg Lys Ile Gln Gly Asp Gly Ala Ala Leu Gln Glu
 195 200 205
 Lys Leu Cys Ala Thr Tyr Lys Leu Cys His Pro Glu Glu Leu Val Leu
 210 215 220
 Leu Gly His Ser Leu Gly Ile Pro Trp Ala Pro Leu Ser Ser Cys Pro
 225 230 235 240
 Ser Gln Ala Leu Gln Leu Ala Gly Cys Leu Ser Gln Leu His Ser Gly
 245 250 255
 Leu Phe Leu Tyr Gln Gly Leu Leu Gln Ala Leu Glu Gly Ile Ser Pro
 260 265 270
 Glu Leu Gly Pro Thr Leu Asp Thr Leu Gln Leu Asp Val Ala Asp Phe
 275 280 285
 Ala Thr Thr Ile Trp Gln Gln Met Glu Glu Leu Gly Met Ala Pro Ala
 290 295 300
 Leu Gln Pro Thr Gln Gly Ala Met Pro Ala Phe Ala Ser Ala Phe Gln
 305 310 315 320
 Arg Arg Ala Gly Gly Val Leu Val Ala Ser His Leu Gln Ser Phe Leu
 325 330 335
 Glu Val Ser Tyr Arg Val Leu Arg His Leu Ala Gln Pro
 340 345

(2) INFORMATION FOR SEQ ID NO:140:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 64 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "synthetic DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:140:

GGATCCACCA TGAGCCGCCT GCCCCGTCTG CTCCCTGCTCC AACTCCTGGT CCGCCCCGCC	60
ATGG	64

(2) INFORMATION FOR SEQ ID NO:141:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 259 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:141:

Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His His Leu Lys
1 5 10 15

Arg Pro Pro Asn Pro Leu Leu Asp Pro Asn Asn Leu Asn Ser Glu Asp
20 25 30

Met Asp Ile Leu Met Glu Arg Asn Leu Arg Thr Pro Asn Leu Leu Ala
35 40 45

Phe Val Arg Ala Val Lys His Leu Glu Asn Ala Ser Gly Ile Glu Ala
50 55 60

Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro
65 70 75 80

Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg
85 90 95

Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu Gln
100 105 110

Gln Tyr Val Ile Glu Gly Arg Ile Ser Pro Gly Gly Ser Gly Gly
115 120 125

Gly Ser Asn Met Ala Pro Ala Arg Ser Pro Ser Pro Ser Thr Gln Pro
130 135 140

Trp Glu His Val Asn Ala Ile Gln Glu Ala Arg Arg Leu Leu Asn Leu
145 150 155 160

Ser Arg Asp Thr Ala Ala Glu Met Asn Glu Thr Val Glu Val Ile Ser
165 170 175

Glu Met Phe Asp Leu Gln Glu Pro Thr Cys Leu Gln Thr Arg Leu Glu
180 185 190

Leu Tyr Lys Gln Gly Leu Arg Gly Ser Leu Thr Lys Leu Lys Gly Pro
195 200 205

Leu Thr Met Met Ala Ser His Tyr Lys Gln His Cys Pro Pro Thr Pro
210 215 220

Glu Thr Ser Cys Ala Thr Gln Ile Ile Thr Phe Glu Ser Phe Lys Glu
225 230 235 240

Asn Leu Lys Asp Phe Leu Leu Val Ile Pro Phe Asp Cys Trp Glu Pro
245 250 255

Val Gln Glu

(2) INFORMATION FOR SEQ ID NO:142:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 301 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:142:

Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His His Leu Lys
1 5 10 15

Arg Pro Pro Asn Pro Leu Leu Asp Pro Asn Asn Leu Asn Ser Glu Asp
20 25 30

Met Asp Ile Leu Met Glu Arg Asn Leu Arg Thr Pro Asn Leu Leu Ala
35 40 45

Phe Val Arg Ala Val Lys His Leu Glu Asn Ala Ser Gly Ile Glu Ala
50 55 60

Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro
65 70 75 80

Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg
85 90 95

Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu Gln
100 105 110

Gln Tyr Val Ile Glu Gly Arg Ile Ser Pro Gln Pro Pro Val Asn Ala
115 120 125

Gly Gly Gly Ser Gly Gly Ser Gly Gly Ser Glu Gly Gly
130 135 140

Ser Glu Gly Gly Ser Glu Gly Gly Ser Glu Gly Gly Ser
145 150 155 160

Gly Gly Gly Ser Gly Ser Gly Asp Phe Asp Tyr Glu Asn Met Ala Pro
165 170 175

Ala Arg Ser Pro Ser Pro Ser Thr Gln Pro Trp Glu His Val Asn Ala
180 185 190

Ile Gln Glu Ala Arg Arg Leu Leu Asn Leu Ser Arg Asp Thr Ala Ala
195 200 205

Glu Met Asn Glu Thr Val Glu Val Ile Ser Glu Met Phe Asp Leu Gln
210 215 220

Glu Pro Thr Cys Leu Gln Thr Arg Leu Glu Leu Tyr Lys Gln Gly Leu
 225 230 235 240
 Arg Gly Ser Leu Thr Lys Leu Lys Gly Pro Leu Thr Met Met Ala Ser
 245 250 255
 His Tyr Lys Gln His Cys Pro Pro Thr Pro Glu Thr Ser Cys Ala Thr
 260 265 270
 Gln Ile Ile Thr Phe Glu Ser Phe Lys Glu Asn Leu Lys Asp Phe Leu
 275 280 285
 Leu Val Ile Pro Phe Asp Cys Trp Glu Pro Val Gln Glu
 290 295 300

(2) INFORMATION FOR SEQ ID NO:143:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 335 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:143:

Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys
 1 5 10 15
 Arg Pro Pro Asn Pro Leu Leu Asp Pro Asn Asn Leu Asn Ser Glu Asp
 20 25 30
 Met Asp Ile Leu Met Glu Arg Asn Leu Arg Thr Pro Asn Leu Leu Ala
 35 40 45
 Phe Val Arg Ala Val Lys His Leu Glu Asn Ala Ser Gly Ile Glu Ala
 50 55 60
 Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro
 65 70 75 80
 Ser Arg His Pro Ile Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg
 85 90 95
 Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu Gln
 100 105 110
 Gln Tyr Val Pro Val Asn Ala Gly Gly Ser Gly Gly Ser Gly
 115 120 125
 Gly Gly Ser Glu Gly Gly Ser Glu Gly Gly Ser Glu Gly Gly
 130 135 140
 Gly Ser Glu Gly Gly Ser Gly Gly Ser Gly Ser Gly Asn Met
 145 150 155 160
 Ala Thr Pro Leu Gly Pro Ala Ser Ser Leu Pro Gln Ser Phe Leu Leu

165	170	175
Lys Cys Leu Glu Gln Val Arg Lys Ile Gln Gly Asp Gly Ala Ala Leu		
180	185	190
Gln Glu Lys Leu Cys Ala Thr Tyr Lys Leu Cys His Pro Glu Glu Leu		
195	200	205
Val Leu Leu Gly His Ser Leu Gly Ile Pro Trp Ala Pro Leu Ser Ser		
210	215	220
Cys Pro Ser Gln Ala Leu Gln Leu Ala Gly Cys Leu Ser Gln Leu His		
225	230	235
Ser Gly Leu Phe Leu Tyr Gln Gly Leu Leu Gln Ala Leu Glu Gly Ile		
245	250	255
Ser Pro Glu Leu Gly Pro Thr Leu Asp Thr Leu Gln Leu Asp Val Ala		
260	265	270
Asp Phe Ala Thr Thr Ile Trp Gln Gln Met Glu Glu Leu Gly Met Ala		
275	280	285
Pro Ala Leu Gln Pro Thr Gln Gly Ala Met Pro Ala Phe Ala Ser Ala		
290	295	300
Phe Gln Arg Arg Ala Gly Gly Val Leu Val Ala Ser His Leu Gln Ser		
305	310	315
Phe Leu Glu Val Ser Tyr Arg Val Leu Arg His Leu Ala Gln Pro		
325	330	335

(2) INFORMATION FOR SEQ ID NO:144:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 274 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:144:

Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His His Leu Lys		
1	5	10
Arg Pro Pro Asn Pro Leu Leu Asp Pro Asn Asn Leu Asn Ser Glu Asp		
20	25	30
Met Asp Ile Leu Met Glu Arg Asn Leu Arg Thr Pro Asn Leu Leu Ala		
35	40	45
Phe Val Arg Ala Val Lys His Leu Glu Asn Ala Ser Gly Ile Glu Ala		
50	55	60
Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro		
65	70	75

Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg
 85 90 95
 Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu Gln
 100 105 110
 Gln Tyr Val Ile Glu Gly Arg Ile Ser Pro Gly Glu Pro Ser Gly Pro
 115 120 125
 Ile Ser Thr Ile Asn Pro Ser Pro Pro Ser Lys Glu Ser His Lys Ser
 130 135 140
 Pro Asn Met Ala Pro Ala Arg Ser Pro Ser Pro Ser Thr Gln Pro Trp
 145 150 155 160
 Glu His Val Asn Ala Ile Gln Glu Ala Arg Arg Leu Leu Asn Leu Ser
 165 170 175
 Arg Asp Thr Ala Ala Glu Met Asn Glu Thr Val Glu Val Ile Ser Glu
 180 185 190
 Met Phe Asp Leu Gln Glu Pro Thr Cys Leu Gln Thr Arg Leu Glu Leu
 195 200 205
 Tyr Lys Gln Gly Leu Arg Gly Ser Leu Thr Lys Leu Lys Gly Pro Leu
 210 215 220
 Thr Met Met Ala Ser His Tyr Lys Gln His Cys Pro Pro Thr Pro Glu
 225 230 235 240
 Thr Ser Cys Ala Thr Gln Ile Ile Thr Phe Glu Ser Phe Lys Glu Asn
 245 250 255
 Leu Lys Asp Phe Leu Leu Val Ile Pro Phe Asp Cys Trp Glu Pro Val
 260 265 270
 Gln Glu

(2) INFORMATION FOR SEQ ID NO:145:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 317 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:145:

Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys
 1 5 10 15
 Arg Pro Pro Asn Pro Leu Leu Asp Pro Asn Asn Leu Asn Ser Glu Asp
 20 25 30

Met Asp Ile Leu Met Glu Arg Asn Leu Arg Thr Pro Asn Leu Leu Ala
 35 40 45
 Phe Val Arg Ala Val Lys His Leu Glu Asn Ala Ser Gly Ile Glu Ala
 50 55 60
 Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro
 65 70 75 80
 Ser Arg His Pro Ile Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg
 85 90 95
 Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu Gln
 100 105 110
 Gln Tyr Val Ile Glu Gly Arg Ile Ser Pro Gly Gly Ser Gly Gly
 115 120 125
 Gly Ser Asn Met Ala Pro Val Pro Pro Gly Glu Asp Ser Lys Asp Val
 130 135 140
 Ala Ala Pro His Arg Gln Pro Leu Thr Ser Ser Glu Arg Ile Asp Lys
 145 150 155 160
 Gln Ile Arg Tyr Ile Leu Asp Gly Ile Ser Ala Leu Arg Lys Glu Thr
 165 170 175
 Cys Asn Lys Ser Asn Met Cys Glu Ser Ser Lys Glu Ala Leu Ala Glu
 180 185 190
 Asn Asn Leu Asn Leu Pro Lys Met Ala Glu Lys Asp Gly Cys Phe Gln
 195 200 205
 Ser Gly Phe Asn Glu Glu Thr Cys Leu Val Lys Ile Ile Thr Gly Leu
 210 215 220
 Leu Glu Phe Glu Val Tyr Leu Glu Tyr Leu Gln Asn Arg Phe Glu Ser
 225 230 235 240
 Ser Glu Glu Gln Ala Arg Ala Val Gln Met Ser Thr Lys Val Leu Ile
 245 250 255
 Gln Phe Leu Gln Lys Lys Ala Lys Asn Leu Asp Ala Ile Thr Thr Pro
 260 265 270
 Asp Pro Thr Thr Asn Ala Ser Leu Leu Thr Lys Leu Gln Ala Gln Asn
 275 280 285
 Gln Trp Leu Gln Asp Met Thr Thr His Leu Ile Leu Arg Ser Phe Lys
 290 295 300
 Glu Phe Leu Gln Ser Ser Leu Arg Ala Leu Arg Gln Met
 305 310 315

(2) INFORMATION FOR SEQ ID NO:146:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 307 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:146:

Met Ala Thr Pro Leu Gly Pro Ala Ser Ser Leu Pro Gln Ser Phe Leu
1 5 10 15

Leu Lys Cys Leu Glu Gln Val Arg Lys Ile Gln Gly Asp Gly Ala Ala
20 25 30

Leu Gln Glu Lys Leu Cys Ala Thr Tyr Lys Leu Cys His Pro Glu Glu
35 40 45

Leu Val Leu Leu Gly His Ser Leu Gly Ile Pro Trp Ala Pro Leu Ser
50 55 60

Ser Cys Pro Ser Gln Ala Leu Gln Leu Ala Gly Cys Leu Ser Gln Leu
65 70 75 80

His Ser Gly Leu Phe Leu Tyr Gln Gly Leu Leu Gln Ala Leu Glu Gly
85 90 95

Ile Ser Pro Glu Leu Gly Pro Thr Leu Asp Thr Leu Gln Leu Asp Val
100 105 110

Ala Asp Phe Ala Thr Thr Ile Trp Gln Gln Met Glu Glu Leu Gly Met
115 120 125

Ala Pro Ala Leu Gln Pro Thr Gln Gly Ala Met Pro Ala Phe Ala Ser
130 135 140

Ala Phe Gln Arg Arg Ala Gly Gly Val Leu Val Ala Ser His Leu Gln
145 150 155 160

Ser Phe Leu Glu Val Ser Tyr Arg Val Leu Arg His Leu Ala Gln Pro
165 170 175

Tyr Val Ile Glu Gly Arg Ile Ser Pro Gly Gly Ser Gly Gly Gly
180 185 190

Ser Asn Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His
195 200 205

Leu Lys Arg Pro Pro Asn Pro Leu Leu Asp Pro Asn Asn Leu Asn Ser
210 215 220

Glu Asp Met Asp Ile Leu Met Glu Arg Asn Leu Arg Thr Pro Asn Leu
225 230 235 240

Leu Ala Phe Val Arg Ala Val Lys His Leu Glu Asn Ala Ser Gly Ile
245 250 255

Glu Ala Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala
260 265 270

Ala Pro Ser Arg His Pro Ile Ile Lys Ala Gly Asp Trp Gln Glu
275 280 285

Phe Arg Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln
290 295 300

Glu Gln Gln
305

(2) INFORMATION FOR SEQ ID NO:147:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 307 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:147:

Met Ala Thr Pro Leu Gly Pro Ala Ser Ser Leu Pro Gln Ser Phe Leu
1 5 10 15

Leu Lys Cys Leu Glu Gln Val Arg Lys Ile Gln Gly Asp Gly Ala Ala
20 25 30

Leu Gln Glu Lys Leu Cys Ala Thr Tyr Lys Leu Cys His Pro Glu Glu
35 40 45

Leu Val Leu Leu Gly His Ser Leu Gly Ile Pro Trp Ala Pro Leu Ser
50 55 60

Ser Cys Pro Ser Gln Ala Leu Gln Leu Ala Gly Cys Leu Ser Gln Leu
65 70 75 80

His Ser Gly Leu Phe Leu Tyr Gln Gly Leu Leu Gln Ala Leu Glu Gly
85 90 95

Ile Ser Pro Glu Leu Gly Pro Thr Leu Asp Thr Leu Gln Leu Asp Val
100 105 110

Ala Asp Phe Ala Thr Thr Ile Trp Gln Gln Met Glu Glu Leu Gly Met
115 120 125

Ala Pro Ala Leu Gln Pro Thr Gln Gly Ala Met Pro Ala Phe Ala Ser
130 135 140

Ala Phe Gln Arg Arg Ala Gly Gly Val Leu Val Ala Ser His Leu Gln
145 150 155 160

Ser Phe Leu Glu Val Ser Tyr Arg Val Leu Arg His Leu Ala Gln Pro
165 170 175

Tyr Val Ile Glu Gly Arg Ile Ser Pro Gly Gly Ser Gly Gly Gly
180 185 190

Ser Asn Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His
195 200 205

Leu Lys Arg Pro Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn Asp
 210 215 220
 Glu Asp Val Ser Ile Leu Met Asp Arg Asn Leu Arg Leu Pro Asn Leu
 225 230 235 240
 Glu Ser Phe Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Gly Ile
 245 250 255
 Glu Ala Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala
 260 265 270
 Ala Pro Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu
 275 280 285
 Phe Arg Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln
 290 295 300
 Glu Gln Gln
 305

(2) INFORMATION FOR SEQ ID NO:148:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 337 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:148:

Met Ala Thr Pro Leu Gly Pro Ala Ser Ser Leu Pro Gln Ser Phe Leu
 1 5 10 15
 Leu Lys Cys Leu Glu Gln Val Arg Lys Ile Gln Gly Asp Gly Ala Ala
 20 25 30
 Leu Gln Glu Lys Leu Cys Ala Thr Tyr Lys Leu Cys His Pro Glu Glu
 35 40 45
 Leu Val Leu Leu Gly His Ser Leu Gly Ile Pro Trp Ala Pro Leu Ser
 50 55 60
 Ser Cys Pro Ser Gln Ala Leu Gln Leu Ala Gly Cys Leu Ser Gln Leu
 65 70 75 80
 His Ser Gly Leu Phe Leu Tyr Gln Gly Leu Leu Gln Ala Leu Glu Gly
 85 90 95
 Ile Ser Pro Glu Leu Gly Pro Thr Leu Asp Thr Leu Gln Leu Asp Val
 100 105 110
 Ala Asp Phe Ala Thr Thr Ile Trp Gln Gln Met Glu Glu Leu Gly Met
 115 120 125
 Ala Pro Ala Leu Gln Pro Thr Gln Gly Ala Met Pro Ala Phe Ala Ser

130

135

140

Ala Phe Gln Arg Arg Ala Gly Gly Val Leu Val Ala Ser His Leu Gln
145 150 155 160

Ser Phe Leu Glu Val Ser Tyr Arg Val Leu Arg His Leu Ala Gln Pro
165 170 175

Tyr Val Pro Gln Pro Pro Val Asn Ala Gly Gly Ser Gly Gly Gly
180 185 190

Ser Gly Gly Ser Glu Gly Gly Ser Glu Gly Gly Ser Gly Ser Glu
195 200 205

Gly Gly Gly Ser Glu Gly Gly Ser Gly Gly Ser Gly Ser Gly
210 215 220

Asp Phe Asp Tyr Glu Asn Met Ala Asn Cys Ser Ile Met Ile Asp Glu
225 230 235 240

Ile Ile His His Leu Lys Arg Pro Pro Ala Pro Leu Leu Asp Pro Asn
245 250 255

Asn Leu Asn Asp Glu Asp Val Ser Ile Leu Met Asp Arg Asn Leu Arg
260 265 270

Leu Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Gly Ile Glu Ala
275 280 285

Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro
290 295 300

Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg
305 310 315 320

Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu Gln
325 330 335

Gln

(2) INFORMATION FOR SEQ ID NO:149:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 322 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:149:

Met Ala Thr Pro Leu Gly Pro Ala Ser Ser Leu Pro Gln Ser Phe Leu
1 5 10 15

Leu Lys Cys Leu Glu Gln Val Arg Lys Ile Gln Gly Asp Gly Ala Ala
20 25 30

Leu Gln Glu Lys Leu Cys Ala Thr Tyr Lys Leu Cys His Pro Glu Glu
 35 40 45
 Leu Val Leu Leu Gly His Ser Leu Gly Ile Pro Trp Ala Pro Leu Ser
 50 55 60
 Ser Cys Pro Ser Gln Ala Leu Gln Leu Ala Gly Cys Leu Ser Gln Leu
 65 70 75 80
 His Ser Gly Leu Phe Leu Tyr Gln Gly Leu Leu Gln Ala Leu Glu Gly
 85 90 95
 Ile Ser Pro Glu Leu Gly Pro Thr Leu Asp Thr Leu Gln Leu Asp Val
 100 105 110
 Ala Asp Phe Ala Thr Thr Ile Trp Gln Gln Met Glu Glu Leu Gly Met
 115 120 125
 Ala Pro Ala Leu Gln Pro Thr Gln Gly Ala Met Pro Ala Phe Ala Ser
 130 135 140
 Ala Phe Gln Arg Arg Ala Gly Gly Val Leu Val Ala Ser His Leu Gln
 145 150 155 160
 Ser Phe Leu Glu Val Ser Tyr Arg Val Leu Arg His Leu Ala Gln Pro
 165 170 175
 Tyr Val Ile Glu Gly Arg Ile Ser Pro Gly Glu Pro Ser Gly Pro Ile
 180 185 190
 Ser Thr Ile Asn Pro Ser Pro Pro Ser Lys Glu Ser His Lys Ser Pro
 195 200 205
 Asn Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu
 210 215 220
 Lys Arg Pro Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn Asp Glu
 225 230 235 240
 Asp Val Ser Ile Leu Met Asp Arg Asn Leu Arg Leu Pro Asn Leu Glu
 245 250 255
 Ser Phe Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Gly Ile Glu
 260 265 270
 Ala Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala Ala
 275 280 285
 Pro Ser Arg His Pro Ile Ile Lys Ala Gly Asp Trp Gln Glu Phe
 290 295 300
 Arg Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu
 305 310 315 320
 Gln Gln

(2) INFORMATION FOR SEQ ID NO:150:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 322 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:150:

Met Ala Thr Pro Leu Gly Pro Ala Ser Ser Leu Pro Gln Ser Phe Leu
1 5 10 15

Leu Lys Cys Leu Glu Gln Val Arg Lys Ile Gln Gly Asp Gly Ala Ala
20 25 30

Leu Gln Glu Lys Leu Cys Ala Thr Tyr Lys Leu Cys His Pro Glu Glu
35 40 45

Leu Val Leu Leu Gly His Ser Leu Gly Ile Pro Trp Ala Pro Leu Ser
50 55 60

Ser Cys Pro Ser Gln Ala Leu Gln Leu Ala Gly Cys Leu Ser Gln Leu
65 70 75 80

His Ser Gly Leu Phe Leu Tyr Gln Gly Leu Leu Gln Ala Leu Glu Gly
85 90 95

Ile Ser Pro Glu Leu Gly Pro Thr Leu Asp Thr Leu Gln Leu Asp Val
100 105 110

Ala Asp Phe Ala Thr Thr Ile Trp Gln Gln Met Glu Glu Leu Gly Met
115 120 125

Ala Pro Ala Leu Gln Pro Thr Gln Gly Ala Met Pro Ala Phe Ala Ser
130 135 140

Ala Phe Gln Arg Arg Ala Gly Gly Val Leu Val Ala Ser His Leu Gln
145 150 155 160

Ser Phe Leu Glu Val Ser Tyr Arg Val Leu Arg His Leu Ala Gln Pro
165 170 175

Tyr Val Ile Glu Gly Arg Ile Ser Pro Gly Glu Pro Ser Gly Pro Ile
180 185 190

Ser Thr Ile Asn Pro Ser Pro Pro Ser Lys Glu Ser His Lys Ser Pro
195 200 205

Asn Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu
210 215 220

Lys Arg Pro Pro Asn Pro Leu Leu Asp Pro Asn Asn Leu Asn Ser Glu
225 230 235 240

Asp Met Asp Ile Leu Met Glu Arg Asn Leu Arg Thr Pro Asn Leu Leu
245 250 255

Ala Phe Val Arg Ala Val Lys His Leu Glu Asn Ala Ser Gly Ile Glu

260

265

270

Ala Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala Ala
275 280 285

Pro Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu Phe
290 295 300

Arg Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu
305 310 315 320

Gln Gln

(2) INFORMATION FOR SEQ ID NO:151:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 349 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:151:

Met Ala Thr Pro Leu Gly Pro Ala Ser Ser Leu Pro Gln Ser Phe Leu
1 5 10 15

Leu Lys Cys Leu Glu Gln Val Arg Lys Ile Gln Gly Asp Gly Ala Ala
20 25 30

Leu Gln Glu Lys Leu Cys Ala Thr Tyr Lys Leu Cys His Pro Glu Glu
35 40 45

Leu Val Leu Leu Gly His Ser Leu Gly Ile Pro Trp Ala Pro Leu Ser
50 55 60

Ser Cys Pro Ser Gln Ala Leu Gln Leu Ala Gly Cys Leu Ser Gln Leu
65 70 75 80

His Ser Gly Leu Phe Leu Tyr Gln Gly Leu Leu Gln Ala Leu Glu Gly
85 90 95

Ile Ser Pro Glu Leu Gly Pro Thr Leu Asp Thr Leu Gln Leu Asp Val
100 105 110

Ala Asp Phe Ala Thr Thr Ile Trp Gln Gln Met Glu Glu Leu Gly Met
115 120 125

Ala Pro Ala Leu Gln Pro Thr Gln Gly Ala Met Pro Ala Phe Ala Ser
130 135 140

Ala Phe Gln Arg Arg Ala Gly Gly Val Leu Val Ala Ser His Leu Gln
145 150 155 160

Ser Phe Leu Glu Val Ser Tyr Arg Val Leu Arg His Leu Ala Gln Pro
165 170 175

Tyr Val Ile Glu Gly Arg Ile Ser Pro Gln Pro Pro Val Asn Ala Gly
180 185 190
Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly Glu Gly Gly Ser
195 200 205
Glu Gly Gly Ser Glu Gly Gly Ser Glu Gly Gly Ser Gly
210 215 220
Gly Gly Ser Gly Ser Gly Asp Phe Asp Tyr Glu Asn Met Ala Asn Cys
225 230 235 240
Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys Arg Pro Pro Asn
245 250 255
Pro Leu Leu Asp Pro Asn Asn Leu Asn Ser Glu Asp Met Asp Ile Leu
260 265 270
Met Glu Arg Asn Leu Arg Thr Pro Asn Leu Leu Ala Phe Val Arg Ala
275 280 285
Val Lys His Leu Glu Asn Ala Ser Gly Ile Glu Ala Ile Leu Arg Asn
290 295 300
Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro Ser Arg His Pro
305 310 315 320
Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg Glu Lys Leu Thr
325 330 335
Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu Gln Gln
340 345

(2) INFORMATION FOR SEQ ID NO:152:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 307 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:152:

Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys
1 5 10 15
Arg Pro Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn Asp Glu Asp
20 25 30
Val Ser Ile Leu Met Asp Arg Asn Leu Arg Leu Pro Asn Leu Glu Ser
35 40 45
Phe Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Gly Ile Glu Ala
50 55 60

Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro
 65 70 75 80
 Ser Arg His Pro Ile Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg
 85 90 95
 Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu Gln
 100 105 110
 Gln Tyr Val Glu Gly Gly Ser Pro Gly Gly Ser Gly Gly
 115 120 125
 Gly Ser Asn Met Ala Thr Pro Leu Gly Pro Ala Ser Ser Leu Pro Gln
 130 135 140
 Ser Phe Leu Leu Lys Ser Leu Glu Gln Val Arg Lys Ile Gln Gly Asp
 145 150 155 160
 Gly Ala Ala Leu Gln Glu Lys Leu Cys Ala Thr Tyr Lys Leu Cys His
 165 170 175
 Pro Glu Glu Leu Val Leu Leu Gly His Ser Leu Gly Ile Pro Trp Ala
 180 185 190
 Pro Leu Ser Ser Cys Pro Ser Gln Ala Leu Gln Leu Ala Gly Cys Leu
 195 200 205
 Ser Gln Leu His Ser Gly Leu Phe Leu Tyr Gln Gly Leu Leu Gln Ala
 210 215 220
 Leu Glu Gly Ile Ser Pro Glu Leu Gly Pro Thr Leu Asp Thr Leu Gln
 225 230 235 240
 Leu Asp Val Ala Asp Phe Ala Thr Thr Ile Trp Gln Gln Met Glu Glu
 245 250 255
 Leu Gly Met Ala Pro Ala Leu Gln Pro Thr Gln Gly Ala Met Pro Ala
 260 265 270
 Phe Ala Ser Ala Phe Gln Arg Arg Ala Gly Gly Val Leu Val Ala Ser
 275 280 285
 His Leu Gln Ser Phe Leu Glu Val Ser Tyr Arg Val Leu Arg His Leu
 290 295 300
 Ala Gln Pro
 305

(2) INFORMATION FOR SEQ ID NO:153:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 244 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:153:

Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys
1 5 10 15

Arg Pro Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn Asp Glu Asp
20 25 30

Val Ser Ile Leu Met Asp Arg Asn Leu Arg Leu Pro Asn Leu Glu Ser
35 40 45

Phe Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Gly Ile Glu Ala
50 55 60

Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro
65 70 75 80

Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg
85 90 95

Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu Gln
100 105 110

Gln Tyr Val Glu Gly Gly Ser Pro Gly Gly Ser Gly Gly
115 120 125

Gly Ser Asn Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His
130 135 140

His Leu Lys Arg Pro Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn
145 150 155 160

Asp Glu Asp Val Ser Ile Leu Met Asp Arg Asn Leu Arg Leu Pro Asn
165 170 175

Leu Glu Ser Phe Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Gly
180 185 190

Ile Glu Ala Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr
195 200 205

Ala Ala Pro Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln
210 215 220

Glu Phe Arg Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala
225 230 235 240

Gln Glu Gln Gln

(2) INFORMATION FOR SEQ ID NO:154:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 322 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:154:

Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys
1 5 10 15

Arg Pro Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn Asp Glu Asp
20 25 30

Val Ser Ile Leu Met Asp Arg Asn Leu Arg Leu Pro Asn Leu Glu Ser
35 40 45

Phe Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Gly Ile Glu Ala
50 55 60

Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro
65 70 75 80

Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg
85 90 95

Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu Gln
100 105 110

Gln Tyr Val Ile Glu Gly Gly Ser Pro Gly Glu Pro Ser Gly Pro
115 120 125

Ile Ser Thr Ile Asn Pro Ser Pro Pro Ser Lys Glu Ser His Lys Ser
130 135 140

Pro Asn Met Ala Thr Pro Leu Gly Pro Ala Ser Ser Leu Pro Gln Ser
145 150 155 160

Phe Leu Leu Lys Ser Leu Glu Gln Val Arg Lys Ile Gln Gly Asp Gly
165 170 175

Ala Ala Leu Gln Glu Lys Leu Cys Ala Thr Tyr Lys Leu Cys His Pro
180 185 190

Glu Glu Leu Val Leu Leu Gly His Ser Leu Gly Ile Pro Trp Ala Pro
195 200 205

Leu Ser Ser Cys Pro Ser Gln Ala Leu Gln Leu Ala Gly Cys Leu Ser
210 215 220

Gln Leu His Ser Gly Leu Phe Leu Tyr Gln Gly Leu Leu Gln Ala Leu
225 230 235 240

Glu Gly Ile Ser Pro Glu Leu Gly Pro Thr Leu Asp Thr Leu Gln Leu
245 250 255

Asp Val Ala Asp Phe Ala Thr Thr Ile Trp Gln Gln Met Glu Glu Leu
260 265 270

Gly Met Ala Pro Ala Leu Gln Pro Thr Gln Gly Ala Met Pro Ala Phe
275 280 285

Ala Ser Ala Phe Gln Arg Arg Ala Gly Gly Val Leu Val Ala Ser His
290 295 300

Leu Gln Ser Phe Leu Glu Val Ser Tyr Arg Val Leu Arg His Leu Ala
305 310 315 320

Gln Pro

(2) INFORMATION FOR SEQ ID NO:155:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 259 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:155:

Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys
1 5 10 15

Arg Pro Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn Asp Glu Asp
20 25 30

Val Ser Ile Leu Met Asp Arg Asn Leu Arg Leu Pro Asn Leu Glu Ser
35 40 45

Phe Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Gly Ile Glu Ala
50 55 60

Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro
65 70 75 80

Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg
85 90 95

Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu Gln
100 105 110

Gln Tyr Val Glu Gly Gly Ser Pro Gly Glu Pro Ser Gly Pro
115 120 125

Ile Ser Thr Ile Asn Pro Ser Pro Pro Ser Lys Glu Ser His Lys Ser
130 135 140

Pro Asn Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His
145 150 155 160

Leu Lys Arg Pro Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn Asp
165 170 175

Glu Asp Val Ser Ile Leu Met Asp Arg Asn Leu Arg Leu Pro Asn Leu
180 185 190

Glu Ser Phe Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Gly Ile
195 200 205

Glu Ala Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala

210

215

220

Ala Pro Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu
225 230 235 240
Phe Arg Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln
245 250 255
Glu Gln Gln

(2) INFORMATION FOR SEQ ID NO:156:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 322 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:156:

Met Ala Thr Pro Leu Gly Pro Ala Ser Ser Leu Pro Gln Ser Phe Leu
1 5 10 15
Leu Lys Cys Leu Glu Gln Val Arg Lys Ile Gln Gly Asp Gly Ala Ala
20 25 30
Leu Gln Glu Lys Leu Cys Ala Thr Tyr Lys Leu Cys His Pro Glu Glu
35 40 45
Leu Val Leu Leu Gly His Ser Leu Gly Ile Pro Trp Ala Pro Leu Ser
50 55 60
Ser Cys Pro Ser Gln Ala Leu Gln Leu Ala Gly Cys Leu Ser Gly Leu
65 70 75 80
His Ser Gly Leu Phe Leu Tyr Gln Gly Leu Leu Gln Ala Leu Glu Gly
85 90 95
Ile Ser Pro Glu Leu Gly Pro Thr Leu Asp Thr Leu Gln Leu Asp Val
100 105 110
Ala Asp Phe Ala Thr Thr Ile Trp Gln Gln Met Glu Glu Leu Gly Met
115 120 125
Ala Pro Ala Leu Gln Pro Thr Gln Gly Ala Met Pro Ala Phe Ala Ser
130 135 140
Ala Phe Gln Arg Arg Ala Gly Gly Val Leu Val Ala Ser His Leu Gln
145 150 155 160
Ser Phe Leu Glu Val Ser Tyr Arg Val Leu Arg His Leu Ala Gln Pro
165 170 175
Tyr Val Glu Gly Gly Ser Pro Gly Glu Pro Ser Gly Pro Ile
180 185 190

Ser Thr Ile Asn Pro Ser Pro Pro Ser Lys Glu Ser His Lys Ser Pro
 195 200 205
 Asn Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu
 210 215 220
 Lys Arg Pro Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn Asp Glu
 225 230 235 240
 Asp Val Ser Ile Leu Met Asp Arg Asn Leu Arg Leu Pro Asn Leu Glu
 245 250 255
 Ser Phe Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Gly Ile Glu
 260 265 270
 Ala Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala Ala
 275 280 285
 Pro Ser Arg His Pro Ile Ile Lys Ala Gly Asp Trp Gln Glu Phe
 290 295 300
 Arg Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu
 305 310 315 320
 Gln Gln

(2) INFORMATION FOR SEQ ID NO:157:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 322 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:157:

Met Ala Thr Pro Leu Gly Pro Ala Ser Ser Leu Pro Gln Ser Phe Leu
 1 5 10 15
 Leu Lys Ser Leu Glu Gln Val Arg Lys Ile Gln Gly Asp Gly Ala Ala
 20 25 30
 Leu Gln Glu Lys Leu Cys Ala Thr Tyr Lys Leu Cys His Pro Glu Glu
 35 40 45
 Leu Val Leu Leu Gly His Ser Leu Gly Ile Pro Trp Ala Pro Leu Ser
 50 55 60
 Ser Cys Pro Ser Gln Ala Leu Gln Leu Ala Gly Cys Leu Ser Gly Leu
 65 70 75 80
 His Ser Gly Leu Phe Leu Tyr Gln Gly Leu Leu Gln Ala Leu Glu Gly
 85 90 95

Ile Ser Pro Glu Leu Gly Pro Thr Leu Asp Thr Leu Gln Leu Asp Val
 100 105 110
 Ala Asp Phe Ala Thr Thr Ile Trp Gln Gln Met Glu Glu Leu Gly Met
 115 120 125
 Ala Pro Ala Leu Gln Pro Thr Gln Gly Ala Met Pro Ala Phe Ala Ser
 130 135 140
 Ala Phe Gln Arg Arg Ala Gly Gly Val Leu Val Ala Ser His Leu Gln
 145 150 155 160
 Ser Phe Leu Glu Val Ser Tyr Arg Val Leu Arg His Leu Ala Gln Pro
 165 170 175
 Tyr Val Glu Gly Gly Ser Pro Gly Glu Pro Ser Gly Pro Ile
 180 185 190
 Ser Thr Ile Asn Pro Ser Pro Pro Ser Lys Glu Ser His Lys Ser Pro
 195 200 205
 Asn Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu
 210 215 220
 Lys Arg Pro Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn Asp Glu
 225 230 235 240
 Asp Val Ser Ile Leu Met Asp Arg Asn Leu Arg Leu Pro Asn Leu Glu
 245 250 255
 Ser Phe Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Gly Ile Glu
 260 265 270
 Ala Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala Ala
 275 280 285
 Pro Ser Arg His Pro Ile Ile Lys Ala Gly Asp Trp Gln Glu Phe
 290 295 300
 Arg Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu
 305 310 315 320
 Gln Gln

(2) INFORMATION FOR SEQ ID NO:158:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 307 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:158:

Met Ala Thr Pro Leu Gly Pro Ala Ser Ser Leu Pro Gln Ser Phe Leu

1

5

10

15

Leu Lys Cys Leu Glu Gln Val Arg Lys Ile Gln Gly Asp Gly Ala Ala
20 25 30

Leu Gln Glu Lys Leu Cys Ala Thr Tyr Lys Leu Cys His Pro Glu Glu
35 40 45

Leu Val Leu Leu Gly His Ser Leu Gly Ile Pro Trp Ala Pro Leu Ser
50 55 60

Ser Cys Pro Ser Gln Ala Leu Gln Leu Ala Gly Cys Leu Ser Gly Leu
65 70 75 80

His Ser Gly Leu Phe Leu Tyr Gln Gly Leu Leu Gln Ala Leu Glu Gly
85 90 95

Ile Ser Pro Glu Leu Gly Pro Thr Leu Asp Thr Leu Gln Leu Asp Val
100 105 110

Ala Asp Phe Ala Thr Thr Ile Trp Gln Gln Met Glu Glu Leu Gly Met
115 120 125

Ala Pro Ala Leu Gln Pro Thr Gln Gly Ala Met Pro Ala Phe Ala Ser
130 135 140

Ala Phe Gln Arg Arg Ala Gly Gly Val Leu Val Ala Ser His Leu Gln
145 150 155 160

Ser Phe Leu Glu Val Ser Tyr Arg Val Leu Arg His Leu Ala Gln Pro
165 170 175

Tyr Val Glu Gly Gly Ser Pro Gly Gly Ser Gly Gly 180 185 190

Ser Asn Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His
195 200 205

Leu Lys Arg Pro Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn Asp
210 215 220

Glu Asp Val Ser Ile Leu Met Asp Arg Asn Leu Arg Leu Pro Asn Leu
225 230 235 240

Glu Ser Phe Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Gly Ile
245 250 255

Glu Ala Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala
260 265 270

Ala Pro Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu
275 280 285

Phe Arg Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln
290 295 300

Glu Gln Gln
305

(2) INFORMATION FOR SEQ ID NO:159:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 307 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:159:

Met Ala Thr Pro Leu Gly Pro Ala Ser Ser Leu Pro Gln Ser Phe Leu
1 5 10 15

Leu Lys Ser Leu Glu Gln Val Arg Lys Ile Gln Gly Asp Gly Ala Ala
20 25 30

Leu Gln Glu Lys Leu Cys Ala Thr Tyr Lys Leu Cys His Pro Glu Glu
35 40 45

Leu Val Leu Leu Gly His Ser Leu Gly Ile Pro Trp Ala Pro Leu Ser
50 55 60

Ser Cys Pro Ser Gln Ala Leu Gln Leu Ala Gly Cys Leu Ser Gly Leu
65 70 75 80

His Ser Gly Leu Phe Leu Tyr Gln Gly Leu Leu Gln Ala Leu Glu Gly
85 90 95

Ile Ser Pro Glu Leu Gly Pro Thr Leu Asp Thr Leu Gln Leu Asp Val
100 105 110

Ala Asp Phe Ala Thr Thr Ile Trp Gln Gln Met Glu Glu Leu Gly Met
115 120 125

Ala Pro Ala Leu Gln Pro Thr Gln Gly Ala Met Pro Ala Phe Ala Ser
130 135 140

Ala Phe Gln Arg Arg Ala Gly Gly Val Leu Val Ala Ser His Leu Gln
145 150 155 160

Ser Phe Leu Glu Val Ser Tyr Arg Val Leu Arg His Leu Ala Gln Pro
165 170 175

Tyr Val Glu Gly Gly Ser Pro Gly Gly Ser Gly Gly Ser Gly Gly
180 185 190

Ser Asn Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His
195 200 205

Leu Lys Arg Pro Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn Asp
210 215 220

Glu Asp Val Ser Ile Leu Met Asp Arg Asn Leu Arg Leu Pro Asn Leu
225 230 235 240

Glu Ser Phe Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Gly Ile
245 250 255

Glu Ala Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala
260 265 270

Ala Pro Ser Arg His Pro Ile Ile Lys Ala Gly Asp Trp Gln Glu
275 280 285

Phe Arg Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln
290 295 300

Glu Gln Gln
305

(2) INFORMATION FOR SEQ ID NO:160:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 128 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:160:

Met Ala Pro Ala Arg Ser Pro Ser Pro Ser Thr Gln Pro Trp Glu His
1 5 10 15

Val Asn Ala Ile Gln Glu Ala Arg Arg Leu Leu Asn Leu Ser Arg Asp
20 25 30

Thr Ala Ala Glu Met Asn Glu Thr Val Glu Val Ile Ser Glu Met Phe
35 40 45

Asp Leu Gln Glu Pro Thr Cys Leu Gln Thr Arg Leu Glu Leu Tyr Lys
50 55 60

Gln Gly Leu Arg Gly Ser Leu Thr Lys Leu Lys Gly Pro Leu Thr Met
65 70 75 80

Met Ala Ser His Tyr Lys Gln His Cys Pro Pro Thr Pro Glu Thr Ser
85 90 95

Cys Ala Thr Gln Ile Ile Thr Phe Glu Ser Phe Lys Glu Asn Leu Lys
100 105 110

Asp Phe Leu Leu Val Ile Pro Phe Asp Cys Trp Glu Pro Val Gln Glu
115 120 125

(2) INFORMATION FOR SEQ ID NO:161:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 176 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:161:

Met Ala Thr Pro Leu Gly Pro Ala Ser Ser Leu Pro Gln Ser Phe Leu
1 5 10 15

Leu Lys Cys Leu Glu Gln Val Arg Lys Ile Gln Gly Asp Gly Ala Ala
20 25 30

Leu Gln Glu Lys Leu Cys Ala Thr Tyr Lys Leu Cys His Pro Glu Glu
35 40 45

Leu Val Leu Leu Gly His Ser Leu Gly Ile Pro Trp Ala Pro Leu Ser
50 55 60

Ser Cys Pro Ser Gln Ala Leu Gln Leu Ala Gly Cys Leu Ser Gln Leu
65 70 75 80

His Ser Gly Leu Phe Leu Tyr Gln Gly Leu Leu Gln Ala Leu Glu Gly
85 90 95

Ile Ser Pro Glu Leu Gly Pro Thr Leu Asp Thr Leu Gln Leu Asp Val
100 105 110

Ala Asp Phe Ala Thr Thr Ile Trp Gln Gln Met Glu Glu Leu Gly Met
115 120 125

Ala Pro Ala Leu Gln Pro Thr Gln Gly Ala Met Pro Ala Phe Ala Ser
130 135 140

Ala Phe Gln Arg Arg Ala Gly Gly Val Leu Val Ala Ser His Leu Gln
145 150 155 160

Ser Phe Leu Glu Val Ser Tyr Arg Val Leu Arg His Leu Ala Gln Pro
165 170 175

(2) INFORMATION FOR SEQ ID NO:162:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 176 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:162:

Met Ala Thr Pro Leu Gly Pro Ala Ser Ser Leu Pro Gln Ser Phe Leu
1 5 10 15

Leu Lys Ser Leu Glu Gln Val Arg Lys Ile Gln Gly Asp Gly Ala Ala
20 25 30

Leu Gln Glu Lys Leu Cys Ala Thr Tyr Lys Leu Cys His Pro Glu Glu
 35 40 45

Leu Val Leu Leu Gly His Ser Leu Gly Ile Pro Trp Ala Pro Leu Ser
 50 55 60

Ser Cys Pro Ser Gln Ala Leu Gln Leu Ala Gly Cys Leu Ser Gln Leu
 65 70 75 80

His Ser Gly Leu Phe Leu Tyr Gln Gly Leu Leu Gln Ala Leu Glu Gly
 85 90 95

Ile Ser Pro Glu Leu Gly Pro Thr Leu Asp Thr Leu Gln Leu Asp Val
 100 105 110

Ala Asp Phe Ala Thr Thr Ile Trp Gln Gln Met Glu Glu Leu Gly Met
 115 120 125

Ala Pro Ala Leu Gln Pro Thr Gln Gly Ala Met Pro Ala Phe Ala Ser
 130 135 140

Ala Phe Gln Arg Arg Ala Gly Gly Val Leu Val Ala Ser His Leu Gln
 145 150 155 160

Ser Phe Leu Glu Val Ser Tyr Arg Val Leu Arg His Leu Ala Gln Pro
 165 170 175

(2) INFORMATION FOR SEQ ID NO:163:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 186 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:163:

Met Ala Pro Val Pro Pro Gly Glu Asp Ser Lys Asp Val Ala Ala Pro
 1 5 10 15

His Arg Gln Pro Leu Thr Ser Ser Glu Arg Ile Asp Lys Gln Ile Arg
 20 25 30

Tyr Ile Leu Asp Gly Ile Ser Ala Leu Arg Lys Glu Thr Cys Asn Lys
 35 40 45

Ser Asn Met Cys Glu Ser Ser Lys Glu Ala Leu Ala Glu Asn Asn Leu
 50 55 60

Asn Leu Pro Lys Met Ala Glu Lys Asp Gly Cys Phe Gln Ser Gly Phe
 65 70 75 80

Asn Glu Glu Thr Cys Leu Val Lys Ile Ile Thr Gly Leu Leu Glu Phe
 85 90 95

Glu Val Tyr Leu Glu Tyr Leu Gln Asn Arg Phe Glu Ser Ser Glu Glu
 100 105 110
 Gln Ala Arg Ala Val Gln Met Ser Thr Lys Val Leu Ile Gln Phe Leu
 115 120 125
 Gln Lys Lys Ala Lys Asn Leu Asp Ala Ile Thr Thr Pro Asp Pro Thr
 130 135 140
 Thr Asn Ala Ser Leu Leu Thr Lys Leu Gln Ala Gln Asn Gln Trp Leu
 145 150 155 160
 Gln Asp Met Thr Thr His Leu Ile Leu Arg Ser Phe Lys Glu Phe Leu
 165 170 175
 Gln Ser Ser Leu Arg Ala Leu Arg Gln Met
 180 185

(2) INFORMATION FOR SEQ ID NO:164:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 155 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:164:

Met Ala Ser Pro Ala Pro Pro Ala Cys Asp Leu Arg Val Leu Ser Lys
 1 5 10 15
 Leu Leu Arg Asp Ser His Val Leu His Ser Arg Leu Ser Gln Cys Pro
 20 25 30
 Glu Val His Pro Leu Pro Thr Pro Val Leu Leu Pro Ala Val Asp Phe
 35 40 45
 Ser Leu Gly Glu Trp Lys Thr Gln Met Glu Glu Thr Lys Ala Gln Asp
 50 55 60
 Ile Leu Gly Ala Val Thr Leu Leu Glu Gly Val Met Ala Ala Arg
 65 70 75 80
 Gln Gln Leu Gly Pro Thr Cys Leu Ser Ser Leu Leu Gly Gln Leu Ser
 85 90 95
 Gly Gln Val Arg Leu Leu Leu Gly Ala Leu Gln Ser Leu Leu Gly Thr
 100 105 110
 Gln Leu Pro Pro Gln Gly Arg Thr Thr Ala His Lys Asp Pro Asn Ala
 115 120 125
 Ile Phe Leu Ser Phe Gln His Leu Leu Arg Gly Lys Val Arg Phe Leu
 130 135 140
 Met Leu Val Gly Gly Ser Thr Leu Cys Val Arg

145

150

155

(2) INFORMATION FOR SEQ ID NO:165:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 286 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:165:

Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys
1 5 10 15

Arg Pro Pro Asn Pro Leu Leu Asp Pro Asn Asn Leu Asn Ser Glu Asp
20 25 30

Met Asp Ile Leu Met Glu Arg Asn Leu Arg Thr Pro Asn Leu Leu Ala
35 40 45

Phe Val Arg Ala Val Lys His Leu Glu Asn Ala Ser Gly Ile Glu Ala
50 55 60

Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro
65 70 75 80

Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg
85 90 95

Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu Gln
100 105 110

Gln Tyr Val Ile Glu Gly Arg Ile Ser Pro Gly Gly Ser Gly Gly
115 120 125

Gly Ser Asn Met Ala Ser Pro Ala Pro Pro Ala Cys Asp Leu Arg Val
130 135 140

Leu Ser Lys Leu Leu Arg Asp Ser His Val Leu His Ser Arg Leu Ser
145 150 155 160

Gln Cys Pro Glu Val His Pro Leu Pro Thr Pro Val Leu Leu Pro Ala
165 170 175

Val Asp Phe Ser Leu Gly Glu Trp Lys Thr Gln Met Glu Glu Thr Lys
180 185 190

Ala Gln Asp Ile Leu Gly Ala Val Thr Leu Leu Leu Glu Gly Val Met
195 200 205

Ala Ala Arg Gln Gln Leu Gly Pro Thr Cys Leu Ser Ser Leu Leu Gly
210 215 220

Gln Leu Ser Gly Gln Val Arg Leu Leu Leu Gly Ala Leu Gln Ser Leu
225 230 235 240

Leu Gly Thr Gln Leu Pro Pro Gln Gly Arg Thr Thr Ala His Lys Asp
245 250 255

Pro Asn Ala Ile Phe Leu Ser Phe Gln His Leu Leu Arg Gly Lys Val
260 265 270

Arg Phe Leu Met Leu Val Gly Gly Ser Thr Leu Cys Val Arg
275 280 285

(2) INFORMATION FOR SEQ ID NO:166:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 286 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:166:

Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys
1 5 10 15

Arg Pro Pro Asn Pro Leu Leu Asp Pro Asn Asn Leu Asn Ser Glu Asp
20 25 30

Met Asp Ile Leu Met Glu Arg Asn Leu Arg Thr Pro Asn Leu Leu Ala
35 40 45

Phe Val Arg Ala Val Lys His Leu Glu Asn Ala Ser Gly Ile Glu Ala
50 55 60

Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro
65 70 75 80

Ser Arg His Pro Ile Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg
85 90 95

Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu Gln
100 105 110

Gln Tyr Val Glu Gly Gly Ser Pro Gly Gly Ser Gly Gly
115 120 125

Gly Ser Asn Met Ala Ser Pro Ala Pro Pro Ala Cys Asp Leu Arg Val
130 135 140

Leu Ser Lys Leu Leu Arg Asp Ser His Val Leu His Ser Arg Leu Ser
145 150 155 160

Gln Cys Pro Glu Val His Pro Leu Pro Thr Pro Val Leu Leu Pro Ala
165 170 175

Val Asp Phe Ser Leu Gly Glu Trp Lys Thr Gln Met Glu Glu Thr Lys
180 185 190

Ala Gln Asp Ile Leu Gly Ala Val Thr Leu Leu Leu Glu Gly Val Met
195 200 205
Ala Ala Arg Gln Gln Leu Gly Pro Thr Cys Leu Ser Ser Leu Leu Gly
210 215 220
Gln Leu Ser Gly Gln Val Arg Leu Leu Leu Gly Ala Leu Gln Ser Leu
225 230 235 240
Leu Gly Thr Gln Leu Pro Pro Gln Gly Arg Thr Thr Ala His Lys Asp
245 250 255
Pro Asn Ala Ile Phe Leu Ser Phe Gln His Leu Leu Arg Gly Lys Val
260 265 270
Arg Phe Leu Met Leu Val Gly Gly Ser Thr Leu Cys Val Arg
275 280 285

(2) INFORMATION FOR SEQ ID NO:167:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 286 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:167:

Met Ala Ser Pro Ala Pro Pro Ala Cys Asp Leu Arg Val Leu Ser Lys
1 5 10 15
Leu Leu Arg Asp Ser His Val Leu His Ser Arg Leu Ser Gln Cys Pro
20 25 30
Glu Val His Pro Leu Pro Thr Pro Val Leu Leu Pro Ala Val Asp Phe
35 40 45
Ser Leu Gly Glu Trp Lys Thr Gln Met Glu Glu Thr Lys Ala Gln Asp
50 55 60
Ile Leu Gly Ala Val Thr Leu Leu Leu Glu Gly Val Met Ala Ala Arg
65 70 75 80
Gln Gln Leu Gly Pro Thr Cys Leu Ser Ser Leu Leu Gly Gln Leu Ser
85 90 95
Gly Gln Val Arg Leu Leu Leu Gly Ala Leu Gln Ser Leu Leu Gly Thr
100 105 110
Gln Leu Pro Pro Gln Gly Arg Thr Thr Ala His Lys Asp Pro Asn Ala
115 120 125
Ile Phe Leu Ser Phe Gln His Leu Leu Arg Gly Lys Val Arg Phe Leu
130 135 140
Met Leu Val Gly Gly Ser Thr Leu Cys Val Arg Tyr Val Ile Glu Gly

145	150	155	160
Arg Ile Ser Pro Gly Gly Gly Ser Gly Gly Ser Asn Met Ala Asn			
165	170	175	
Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys Arg Pro Pro			
180	185	190	
Asn Pro Leu Leu Asp Pro Asn Asn Leu Asn Ser Glu Asp Met Asp Ile			
195	200	205	
Leu Met Glu Arg Asn Leu Arg Thr Pro Asn Leu Leu Ala Phe Val Arg			
210	215	220	
Ala Val Lys His Leu Glu Asn Ala Ser Gly Ile Glu Ala Ile Leu Arg			
225	230	235	240
Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro Ser Arg His			
245	250	255	
Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg Glu Lys Leu			
260	265	270	
Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu Gln Gln			
275	280	285	

(2) INFORMATION FOR SEQ ID NO:168:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 290 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:168:

Met Ala Ser Pro Ala Pro Pro Ala Cys Asp Leu Arg Val Leu Ser Lys			
1	5	10	15
Leu Leu Arg Asp Ser His Val Leu His Ser Arg Leu Ser Gln Cys Pro			
20	25	30	
Glu Val His Pro Leu Pro Thr Pro Val Leu Leu Pro Ala Val Asp Phe			
35	40	45	
Ser Leu Gly Glu Trp Lys Thr Gln Met Glu Glu Thr Lys Ala Gln Asp			
50	55	60	
Ile Leu Gly Ala Val Thr Leu Leu Leu Glu Gly Val Met Ala Ala Arg			
65	70	75	80
Gln Gln Leu Gly Pro Thr Cys Leu Ser Ser Leu Leu Gly Gln Leu Ser			
85	90	95	
Gly Gln Val Arg Leu Leu Leu Gly Ala Leu Gln Ser Leu Leu Gly Thr			
100	105	110	

Gln Leu Pro Pro Gln Gly Arg Thr Thr Ala His Lys Asp Pro Asn Ala
 115 120 125
 Ile Phe Leu Ser Phe Gln His Leu Leu Arg Gly Lys Val Arg Phe Leu
 130 135 140
 Met Leu Val Gly Gly Ser Thr Leu Cys Val Arg Glu Phe His Ala Tyr
 145 150 155 160
 Val Glu Gly Gly Ser Pro Gly Gly Ser Gly Gly Ser
 165 170 175
 Asn Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu
 180 185 190
 Lys Arg Pro Pro Asn Pro Leu Leu Asp Pro Asn Asn Leu Asn Ser Glu
 195 200 205
 Asp Met Asp Ile Leu Met Glu Arg Asn Leu Arg Thr Pro Asn Leu Leu
 210 215 220
 Ala Phe Val Arg Ala Val Lys His Leu Glu Asn Ala Ser Gly Ile Glu
 225 230 235 240
 Ala Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala Ala
 245 250 255
 Pro Ser Arg His Pro Ile Ile Lys Ala Gly Asp Trp Gln Glu Phe
 260 265 270
 Arg Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu
 275 280 285
 Gln Gln
 290

(2) INFORMATION FOR SEQ ID NO:169:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 45 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "synthetic DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:169:

ACGTCCATGG CNTCNCNGC NCCNCCTGCT TGTGACCTCC GAGTC

45

(2) INFORMATION FOR SEQ ID NO:170:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 34 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "synthetic DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:170:

AATAGCTGAA TTCTTACCCCT TCCTGAGACA GATT

34

(2) INFORMATION FOR SEQ ID NO:171:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "synthetic DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:171:

TGACAAGCTT ACCTGACGCA GAGGGTGGAC CCT

33

(2) INFORMATION FOR SEQ ID NO:172:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "synthetic DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:172:

ATGCACGAAT TCCCTGACGC AGAGGGTGGGA

30

(2) INFORMATION FOR SEQ ID NO:173:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "synthetic DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:173:

AATTCCATGC ATAC

14

(2) INFORMATION FOR SEQ ID NO:174:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:174:

GGTACGTATG

10

(2) INFORMATION FOR SEQ ID NO:175:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 561 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:175:

ATGGCTCCAG TACCACCAAGG TGAAGATTCC AAAGATGTGG CCGCCCCACA CAGACAGCCA	60
CTCACCTCTT CAGAACGAAT TGACAAACAA ATTGGTACA TCCTCGACGG GATATCAGCC	120
CTGAGAAAGG AGACATGTAA CAAGAGTAAC ATGTGTGAAA GCAGCAAAGA GGCCTAGCA	180
AAAAACAACC TGAACCTTCC AAAGATGGCT GAAAAAGATG GATGCTTCCA ATCCGGATTC	240
AATGAGGAGA CTTGCCTGGT GAAAATCATC ACTGGTCTTT TGGAGTTGA GGTATACCTC	300
GAGTACCTCC AGAACAGATT TGAGAGTAGT GAGGAACAAG CCAGAGCTGT GCAGATGTCG	360
ACAAAAGTCC TGATCCAGTT CCTGCAGAAA AAGGCAAAGA ATCTAGATGC AATAACCACC	420
CCTGACCCAA CCACAAATGC ATCCCTGCTG ACGAAGCTGC AGGCACAGAA CCAGTGGCTG	480
CAGGACATGA CAACTCATCT CATTCTGCAG AGCTTTAAGG AGTCCTGCA GTCCAGCCTG	540
AGGGCTCTTC GGCAAATGTA G	561

(2) INFORMATION FOR SEQ ID NO:176:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 402 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:176:

ATGGCACCGG CTCGTTCCCC GTCCCCGTCT ACCCAGCCGT GGGAACACGT GAATGCCATC	60
CAGGAGGCC C GCGTCTCCT GAACCTGAGT AGAGACACTG CTGCTGAGAT GAATGAAACA	120
GTAGAAAGTGA TATCAGAAAT GTTTGACCTC CAGGAGCCGA CTTGCCTACA GACCCGCCTG	180
GAGCTGTACA AGCAGGGCCT GCGGGGCAGC CTCACCAAGC TCAAGGGCCC CTTGACCATG	240
ATGGCCAGCC ACTACAAGCA GCACTGCCCT CCAACCCGG AAACTTCTG TGCAACCCAG	300
ATTATCACCT TTGAAAGTTT CAAAGAGAAC CTGAAGGACT TCCTGCTTGT CATCCCCTTT	360
GAUTGCTGGG AGCCAGTCCA GGAGTGATAA GGATCCGAAT TC	402

(2) INFORMATION FOR SEQ ID NO:177:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 546 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:177:

ATGGCTACAC CATTAGGCC C TGCCAGCTCC CTGCCCCAGA GCTTCCTGCT CAAGTGCTTA	60
GAGCAAGTGA GGAAGATCCA GGGCGATGGC GCAGCGCTCC AGGAGAAAGCT GTGTGCCACC	120
TACAAGCTGT GCCACCCCGA GGAGCTGGTG CTGCTCGGAC ACTCTCTGGG CATCCCCTGG	180
GCTCCCTGA GCTCCTGCC CAGCCAGGCC CTGCAGCTGG CAGGCTGCTT GAGCCAACTC	240
CATAGCGGCC TTTTCCTCTA CCAGGGGCTC CTGCAGGCC C TGGAAGGGAT ATCCCCCGAG	300
TTGGGTCCCA CCTTGGACAC ACTGCAGCTG GACGTCGCCG ACTTTGCCAC CACCATCTGG	360
CAGCAGATGG AAGAACTGGG AATGGCCCT GCCCTGCAGC CCACCCAGGG TGCCATGCCG	420
GCCTTCGCCT CTGCTTCCA GCGCCGGGCA GGAGGGTCC TGGTTGCTAG CCATCTGCAG	480
AGCTTCCTGG AGGTGTCGTA CCGCGTTCTA CGCCACCTTG CGCAGCCCTG ATAAGGATCC	540
GAATTC	546

(2) INFORMATION FOR SEQ ID NO:178:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 546 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:178:

ATGGCTACAC CATTAGGACC TGCCAGCTCC CTGCCCCAGA GCTTCCTGCT CAAGTGCTTA	60
GAGCAAGTGA GGAAGATCCA GGGCGATGGC GCAGCGCTCC AGGAGAACGCT GTGTGCCACC	120
TACAAGCTGT GCCACCCCGA GGAGCTGGTG CTGCTCGGAC ACTCTCTGGG CATCCCCTGG	180
GCTCCCTGA GCTCCTGCC CAGCCAGGCC CTGCAGCTGG CAGGCTGCTT GAGCCAACTC	240
CATAGCGGCC TTTTCCTCTA CCAGGGGCTC CTGCAGGCC TGGAAGGGAT ATCCCCCGAG	300
TTGGGTCCCA CCTTGGACAC ACTGCAGCTG GACGTCGCCG ACTTTGCCAC CACCATCTGG	360
CAGCAGATGG AAGAACTGGG AATGGCCCT GCCCTGCAGC CCACCCAGGG TGCCATGCCG	420
GCCTTCGCCT CTGCTTCCA GCGCCGGGCA GGAGGGGTCC TGGTTGCTAG CCATCTGCAG	480
AGCTTCCTGG AGGTGTCGTA CCGCGTTCTA CGCCACCTTG CGCAGCCCTG ATAAGGATCC	540
GAATTC	546

(2) INFORMATION FOR SEQ ID NO:179:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 546 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:179:

ATGGCTACAC CATTGGGCC TGCCAGCTCC CTGCCCCAGA GCTTCCTGCT CAAGTCTTTA	60
GAGCAAGTGA GGAAGATCCA GGGCGATGGC GCAGCGCTCC AGGAGAACGCT GTGTGCCACC	120
TACAAGCTGT GCCACCCCGA GGAGCTGGTG CTGCTCGGAC ACTCTCTGGG CATCCCCTGG	180
GCTCCCTGA GCTCCTGCC CAGCCAGGCC CTGCAGCTGG CAGGCTGCTT GAGCCAACTC	240
CATAGCGGCC TTTTCCTCTA CCAGGGGCTC CTGCAGGCC TGGAAGGGAT ATCCCCCGAG	300
TTGGGTCCCA CCTTGGACAC ACTGCAGCTG GACGTCGCCG ACTTTGCCAC CACCATCTGG	360

CAGCAGATGG AAGAACTGGG AATGGCCCT GCCCTGCAGC CCACCCAGGG TGCCATGCCG	420
GCCTTCGCCT CTGCTTCCA GCGCCGGCA GGAGGGGTCC TGGTTGCTAG CCATCTGCAG	480
AGCTTCTGG AGGTGTCGTA CCGCGTTCTA CGCCACCTTG CGCAGCCCTG ATAAGGATCC	540
GAATTC	546

(2) INFORMATION FOR SEQ ID NO:180:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 465 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:180:

ATGGCGTCTC CGGCGCCGCC TGCTTGTGAC CTCCGAGTCC TCAGTAAACT GCTTCGTGAC	60
TCCCCATGTCC TTCACAGCAG ACTGAGCCAG TGCCCAGAGG TTCACCCCTT GCCTACACCT	120
GTCCTGCTGC CTGCTGTGGA CTTTAGCTTG GGAGAATGGA AAACCCAGAT GGAGGAGACC	180
AAGGCACAGG ACATTCTGGG AGCAGTGACC CTTCTGCTGG AGGGAGTGAT GGCAGCACGG	240
GGACAACCTGG GACCCACTTG CCTCTCATCC CTCCTGGGGC AGCTTCTGG ACAGGTCCGT	300
CTCCTCCTTG GGGCCCTGCA GAGCCTCCTT GGAACCCAGC TTCCTCCACA GGGCAGGACC	360
ACAGCTCACA AGGATCCCAA TGCCATCTTC CTGAGCTTCC AACACCTGCT CCGAGGAAAG	420
GTGCGTTTCC TGATGCTTGT AGGAGGGTCC ACCCTCTGCG TCAGG	465

(2) INFORMATION FOR SEQ ID NO:181:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 143 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:181:

CCTGTCAACC CGGGCGGCAGG CTCTGGTGGT GGTTCTGGTG GCGGCTCTGA GGGTGGCGGC	60
TCTGAGGGTG GCGGTTCTGA GGGTGGCGGC TCTGAGGGTG GCGGTTCCGG TGGCGGCTCC	120
GGTTCCGGTA ACATGTATTA TGA	143

(2) INFORMATION FOR SEQ ID NO:182:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 180 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:182:

ATCGTCTGAC CTCCCGGGCC TCCTGTCAAT GCTGGCGCG GCTCTGGTGG TGTTCTGGT	60
GGCGGCTCTG AGGGTGGCGG CTCTGAGGGT GGCGGTTCTG AGGGTGGCGG CTCTGAGGGT	120
GGCGGTTCCG GTGGCGGCTC CGGTTCCGGT GATTTGATT ATGAAAACAT GTCAAACGCT	180

(2) INFORMATION FOR SEQ ID NO:183:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 858 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:183:

ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTAAC	60
CCTTGCTGG ACCCGAACAA CCTCAATTCT GAAGACATGG ATATCCTGAT GGAACGAAAC	120
CTTCGAACTC CAAACCTGCT CGCATTGTA AGGGCTGTCA AGCACTTAGA AAATGCATCA	180
GGTATTGAGG CAATTCTCG TAATCTCAA CCATGTCTGC CCTCTGCCAC GGCGCACCC	240
TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG	300
TTCTATCTGG TTACCCCTGGA GCAAGCGCAG GAACAACAGT ACGTAATCGA GGGAAAGGATT	360
TCCCCGGGTG GTGGTTCTGG CGGCGGCTCC AACATGGCGT CTCCGGCGCC GCCTGCTTGT	420
GACCTCCGAG TCCTCAGTAA ACTGCTTCGT GACTCCCAGT TCCTTCACAG CAGACTGAGC	480
CAGTGCCCAG AGGTTCACCC TTTGCCTACA CCTGTCCTGC TGCCTGCTGT GGACTTTAGC	540
TTGGGAGAAT GGAAAACCCA GATGGAGGAG ACCAAGGCAC AGGACATTCT GGGAGCAGTG	600
ACCCTTCTGC TGGAGGGAGT GATGGCAGCA CGGGGACAAC TGGGACCCAC TTGCCTCTCA	660
TCCCTCCTGG GGCAGCTTTC TGGACAGGTC CGTCTCCTCC TTGGGGCCCT GCAGAGCCTC	720

CTTGGAACCC AGCTTCCTCC ACAGGGCAGG ACCACAGCTC ACAAGGATCC CAATGCCATC	780
TTCCTGAGCT TCCAACACCT GCTCCGAGGA AAGGTGCGTT TCCTGATGCT TGTAGGAGGG	840
TCCACCCTCT GCGTCAGG	858

(2) INFORMATION FOR SEQ ID NO:184:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 858 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:184:

ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTAAC	60
CCTTTGCTGG ACCCGAACAA CCTCAATTCT GAAGACATGG ATATCCTGAT GGAACGAAAC	120
CTTCGAACTC CAAACCTGCT CGCATTGTA AGGGCTGTCA AGCACTTAGA AAATGCATCA	180
GGTATTGAGG CAATTCTTCG TAATCTCAA CCATGTCTGC CCTCTGCCAC GGCGCACCC	240
TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG	300
TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAGT ACGTAGAGGG CGGTGGAGGC	360
TCCCCGGGTG GTGGTTCTGG CGGCGGCTCC AACATGGCGT CTCCGGGCC GCCTGCTTGT	420
GACCTCCGAG TCCTCAGTAA ACTGCTTCGT GACTCCCATG TCCTTCACAG CAGACTGAGC	480
CAGTGCCAG AGGTTCACCC TTTGCCTACA CCTGTCCTGC TGCCTGCTGT GGACTTTAGC	540
TTGGGAGAAT GGAAAACCCA GATGGAGGAG ACCAAGGCAC AGGACATTCT GGGAGCAGTG	600
ACCCCTCTGC TGGAGGGAGT GATGGCAGCA CGGGGACAAC TGGGACCCAC TTGCCTCTCA	660
TCCCTCCTGG GGCAGCTTTC TGGACAGGTC CGTCTCCTCC TTGGGGCCCT GCAGAGCCTC	720
CTTGGAACCC AGCTTCCTCC ACAGGGCAGG ACCACAGCTC ACAAGGATCC CAATGCCATC	780
TTCCTGAGCT TCCAACACCT GCTCCGAGGA AAGGTGCGTT TCCTGATGCT TGTAGGAGGG	840
TCCACCCTCT GCGTCAGG	858

(2) INFORMATION FOR SEQ ID NO:185:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 852 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:185:

ATGGCGTCTC CGGCGCCGCC TGCTTGTGAC CTCCGAGTCC TCAGTAAACT GCTTCGTGAC	60
TCCCCATGTCC TTCACAGCAG ACTGAGCCAG TGCCCAGAGG TTCACCCCTT GCCTACACCT	120
GTCCTGCTGC CTGCTGTGGA CTTTAGCTTG GGAGAATGGA AAACCCAGAT GGAGGAGACC	180
AAGGCACAGG ACATTCTGGG AGCAGTGACC CTTCTGCTGG AGGGAGTGAT GGCAGCACGG	240
GGACAACTGG GACCCACTTG CCTCTCATCC CTCCTGGGGC AGCTTCTGG ACAGGTCCGT	300
CTCCTCCTTG GGGCCCTGCA GAGCCTCCTT GGAACCCAGC TTCCTCCACA GGGCAGGACC	360
ACAGCTCACA AGGATCCCAA TGCCATCTTC CTGAGCTTCC AACACCTGCT CCGAGGAAAG	420
GTGCGTTCC TGATGCTTGT AGGAGGGTCC ACCCTCTGCG TCAGGATCGA GGGAGGATT	480
TCCCCGGGTG GTGGTTCTGG CGGGGGCTCC AACATGGCTA ACTGCTCTAT AATGATCGAT	540
GAAATTATAC ATCACTTAAA GAGACCACCT AACCCCTTGC TGGACCCGAA CAACCTCAAT	600
TCTGAAGACA TGGATATCCT GATGGAACGA AACCTTCGAA CTCCAAACCT GCTCGCATT	660
GTAAGGGCTG TCAAGCACTT AGAAAATGCA TCAGGTATTG AGGCAATTCT TCGTAATCTC	720
CAACCATGTC TGCCCTCTGC CACGGCCGCA CCCTCTCGAC ATCCAATCAT CATCAAGGCA	780
GGTGACTGGC AAGAATTCCG GGAAAAACTG ACGTTCTATC TGGTTACCCCT TGAGCAAGCG	840
CAGGAACAAAC AG	852

(2) INFORMATION FOR SEQ ID NO:186:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 870 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:186:

ATGGCGTCTC CGGCGCCGCC TGCTTGTGAC CTCCGAGTCC TCAGTAAACT GCTTCGTGAC	60
TCCCCATGTCC TTCACAGCAG ACTGAGCCAG TGCCCAGAGG TTCACCCCTT GCCTACACCT	120
GTCCTGCTGC CTGCTGTGGA CTTTAGCTTG GGAGAATGGA AAACCCAGAT GGAGGAGACC	180
AAGGCACAGG ACATTCTGGG AGCAGTGACC CTTCTGCTGG AGGGAGTGAT GGCAGCACGG	240
GGACAACTGG GACCCACTTG CCTCTCATCC CTCCTGGGGC AGCTTCTGG ACAGGTCCGT	300
CTCCTCCTTG GGGCCCTGCA GAGCCTCCTT GGAACCCAGC TTCCTCCACA GGGCAGGACC	360

ACAGCTCACA AGGATCCCAA TGCCATCTTC CTGAGCTTCC AACACCTGCT CCGAGGAAAG 420
GTGCGTTCC TGATGCTTGT AGGAGGGTCC ACCCTCTGCG TCAGGGAATT CCATGCATAC 480
GTAGAGGGCG GTGGAGGCTC CCCGGGTGGT GGTTCTGGCG GCGGCTCCAA CATGGCTAAC 540
TGCTCTATAA TGATCGATGA AATTATACAT CACTTAAAGA GACCACCTAA CCCTTGCTG 600
GACCCGAACA ACCTCAATTG TGAAGACATG GATATCCTGA TGGAACGAAA CCTTCGAAC 660
CCAAACCTGC TCGCATTCTGT AAGGGCTGTC AAGCACTTAG AAAATGCATC AGGTATTGAG 720
GCAATTCTTC GTAATCTCCA ACCATGTCTG CCCTCTGCCA CGGCCGCACC CTCTCGACAT 780
CCAATCATCA TCAAGGCAGG TGACTGGCAA GAATTCCGGG AAAAACTGAC GTTCTATCTG 840
GTTACCCTTG AGCAAGCGCA GGAACAACAG 870

(2) INFORMATION FOR SEQ ID NO:187:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:187:

Met Ser Arg Leu Pro Val Leu Leu Leu Leu Gln Leu Leu Val Arg Pro
1 5 10 15
Ala Met

(2) INFORMATION FOR SEQ ID NO:188:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:188:

Tyr Val Ile Glu Gly Arg Ile Ser Pro Gly Gly Gly Ser Gly Gly Gly
1 5 10 15
Ser Asn

(2) INFORMATION FOR SEQ ID NO:189:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:189:

Tyr Val Ile Glu Gly Lys Ile Ser Pro Gly Gly Ser Gly Gly Gly
1 5 10 15
Ser Asn

(2) INFORMATION FOR SEQ ID NO:190:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:190:

Tyr Val Glu Gly Gly Gly Ser Pro Gly Gly Ser Gly Gly Gly
1 5 10 15
Ser Asn

(2) INFORMATION FOR SEQ ID NO:191:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 33 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:191:

Tyr Val Ile Glu Gly Arg Ile Ser Pro Gly Glu Pro Ser Gly Pro Ile
1 5 10 15
Ser Thr Ile Asn Pro Ser Pro Pro Ser Lys Glu Ser His Lys Ser Pro

Asn

(2) INFORMATION FOR SEQ ID NO:192:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:192:

Tyr Val Ile Glu Gly Lys Ile Ser Pro Gly Glu Pro Ser Gly Pro Ile
1 5 10 15

Ser Thr Ile Asn Pro Ser Pro Pro Ser Lys Glu Ser His Lys Ser Pro
20 25 30

Asn

(2) INFORMATION FOR SEQ ID NO:193:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:193:

Tyr Val Glu Gly Gly Gly Ser Pro Gly Glu Pro Ser Gly Pro Ile
1 5 10 15

Ser Thr Ile Asn Pro Ser Pro Pro Ser Lys Glu Ser His Lys Ser Pro
20 25 30

Asn

(2) INFORMATION FOR SEQ ID NO:194:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 49 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:194:

Tyr Val Ile Glu Gly Arg Ile Ser Pro Gly Gly Gly Ser Gly Gly Gly
1 5 10 15
Ser Gly Gly Ser Glu Gly Gly Ser Glu Gly Gly Ser Glu
20 25 30
Gly Gly Gly Ser Glu Gly Gly Ser Gly Gly Ser Gly Ser Gly
35 40 45

Asn

(2) INFORMATION FOR SEQ ID NO:195:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:195:

Tyr Val Ile Glu Gly Arg Ile Ser Pro Gln Pro Pro Val Asn Ala Gly
1 5 10 15
Gly Gly Ser Gly Gly Ser Gly Gly Ser Glu Gly Gly Ser
20 25 30
Glu Gly Gly Ser Glu Gly Gly Ser Glu Gly Gly Ser Gly
35 40 45
Gly Gly Ser Gly Ser Gly Asp Phe Asp Tyr Glu Asn
50 55 60

(2) INFORMATION FOR SEQ ID NO:196:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:196:

Glu Phe His Ala Tyr Val Glu Gly Gly Gly Ser Pro Gly Gly Gly
1 5 10 15
Ser Gly Gly Ser Asn
20

(2) INFORMATION FOR SEQ ID NO:197:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 408 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:197

ATGGCTCCAA	TGACTCAGAC	TACTTCTCTT	AAGACTTCTT	GGGTTAACTG	CTCTAACATG	60
ATCGATGAAA	TTATAACACA	CTTAAAGCAG	CCACCTTTGC	CTTGCTGGA	CTTCAACAAAC	120
CTCAATGGGG	AAGACCAAGA	CATTCTGATG	GAAAATAACC	TTCGAAGGCC	AAACCTGGAG	180
GCATTCAACA	GGGCTGTCAA	GAGTTTACAG	AATGCATCAG	CAATTGAGAG	CATTCTTAAA	240
AATCTCCTGC	CATGTCTGCC	CCTGGCCACG	GCCGCACCCA	CGCGACATCC	AATCCATATC	300
AAGGACGGTG	ACTGGAATGA	ATTCCGTCGT	AAACTGACCT	TCTATCTGAA	AACCTTGGAG	360
AACGCGCAGG	CTCAACAGAC	CACTCTGTCG	CTAGCGATCT	TTTAATAA		408